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(54) Method for producing nucleoside-5'-phosphate ester

(57) A method for producing nucleoside-5'-phosphate ester involves phosphorylating nucleoside biochemically.

Nucleoside-5'-phosphate ester is produced by allowing an acid phosphatase, especially an acid phosphatase having an increased affinity for a nucleoside and/or an increased temperature stability, to act at pH 3.0 to 5.5 on a nucleoside and a phosphate group donor.

The phosphate group donor may be selected from polyphosphoric acid or a salt thereof, phenylphosphoric acid or a salt thereof, and carbamyl phosphate or a salt thereof. The resulting nucleoside-5'-phosphate ester may subsequently be collected. As an alternative to using isolated acid phosphatase to catalyse the reaction, a microorganism transformed with a gene encoding a protein having acid phosphatase activity may be employed.

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Description

The present invention relates to a method for producing nucleoside-5'-phosphate ester. The present invention also relates to a novel acid phosphatase, a gene coding for the acid phosphatase, a recombinant DNA containing the gene, and a microorganism harboring the recombinant DNA which are useful to produce nucleoside-5'-phosphate ester. Nucleoside-5'-phosphate ester is useful as a seasoning, a pharmaceutical, and a raw material for producing such substances.

Methods for biochemically phosphorylating nucleoside to produce nucleoside-5'-phosphate ester by using the following phosphate group donors are known, including a method which uses p-nitrophenylphosphoric acid (Japanese Patent Publication No. 39-29858), a method which uses inorganic phosphoric acid (Japanese Patent Publication No. 42-1186), a method which uses polyphosphoric acid (Japanese Patent Laid-open No. 53-56390), a method which uses acetylphosphoric acid (Japanese Patent Laid-open No. 56-82098), and a method which uses adenosine triphosphate (ATP) (Japanese Patent Laid-open No. 63-230094). However, these methods have not been satisfactory to produce nucleoside-5'-phosphate ester efficiently and inexpensively because the substrates to be used are expensive, or because by-products are produced in the reaction.

Thus the present inventors have developed a method for efficiently producing nucleoside-5'-phosphate ester without by-producing 2', 3'-nucleotide isomers by allowing cells of a specified microorganism to act under an acidic condition on a nucleoside and a phosphate group donor selected from the group consisting of polyphosphoric acid or a salt thereof, phenylphosphoric acid or a salt thereof, and carbamyl phosphate or a salt thereof (Japanese Patent Laid-open No. 7-231793).

However, even this method has had the following drawbacks. Namely, for example, a part of the substrate is degraded during the reaction due to a nucleoside-degrading activity which unfortunately exists in a slight amount in the cells of the microorganism to be used. Moreover, if the reaction is continued, produced and accumulated nucleoside-5'-phosphate ester is degraded. Therefore, by-products are produced in a reaction solution, and it has been impossible to obtain a sufficient yield. In addition, the reaction cannot be performed if the substrate is added at a high concentration because of a low transphosphorylation activity per microbial cell.

In one embodiment, the present invention desirably provides a method for inexpensively and efficiently producing nucleoside-5'-phosphate ester. According to other embodiments of the present invention there are provided an enzyme, a gene coding for the enzyme, a recombinant DNA containing the gene, and a microorganism harboring the recombinant DNA which are useful for the method for producing nucleoside-5'-phosphate ester.

As a result of various investigations made by the present inventors in order to develop a method for producing nucleoside-5'-phosphate ester which is more efficient than the conventional methods, it has been found out that nucleoside-5'-phosphate ester maybe efficiently produced at a high yield by allowing an acid phosphatase purified from a cell-free extract of a microorganism to act under a condition of pH 3.0 to 5.5 on a nucleoside and a phosphate group donor selected from the group consisting of polyphosphoric acid or a salt thereof, phenylphosphoric acid or a salt thereof, and carbamyl phosphate or a salt thereof. Further, the present inventors have succeeded in obtaining wild type genes coding for acid phosphatases from various bacteria and genes coding for acid phosphatases having an increased affinity for the nucleoside as compared with the wild type acid phosphatase by introducing a mutation into an acid phosphatase derived from a bacterium belonging to the genus *Escherichia*. Moreover, the present inventors have found out that productivity of nucleoside-5'-phosphate ester may be remarkably improved by expressing the gene in a large amount in accordance with genetic engineering techniques.

Further the present inventors have tried to prepare a mutant acid phosphatase with an increased temperature stability, with the intention that conducting a phosphate transfer reaction using the acid phosphatase at a higher temperature leads to a much more effective production of nucleoside-5'-phosphate because the reaction speed is elevated and the concentration of phosphate receiver in the reaction solution can be higher. Then the present inventors have succeeded in the preparation of a mutant acid phosphatase which has an increased temperature stability over mutant acid phosphatases described in Example 19 and can be employed in a reaction at a high temperature, and completed the present invention

Namely, the present invention provides a method for producing nucleoside-5'-phosphate ester comprising the steps of allowing an acid phosphatase having an increased affinity for a nucleoside and/or an increased temperature stability to act under a condition of pH 3.0 to 5.5 on a nucleoside and a phosphate group donor, preferably selected from the group consisting of polyphosphoric acid or a salt thereof, phenylphosphoric acid or a salt thereof, acetylphosphoric acid or a salt thereof, and carbamyl phosphate or a salt thereof to produce nucleoside-5'-phosphate ester, and collecting it.

The term "acid phosphatase having an increased affinity for nucleoside" encompasses those acid phosphatases in which the affinity for nucleoside is higher in comparison with the wild type acid phosphatase. Preferred acid phosphatases have a Michaelis constant, Km, for transphosphorylation of the nucleoside, which is below 100mM.

The term "acid phosphatase having increase temperature stability" encompasses those acid phosphatases which

retain more residual activity after treatment at elevated temperature than does a corresponding wild type acid phosphatase. Preferably, the acid phosphatase retains more activity than the wild type after being held at 50°C for 30 minutes at pH 7.0. Particularly preferably, the acid phosphatase shows substantially no decrease in activity on treatment for 30 minutes at 50°C and pH 7.0.

5 In another aspect, the present invention provides a method for producing nucleoside-5'-phosphate ester comprising the steps of allowing a microorganism to act under a condition of pH 3.0 to 5.5 on a nucleoside and a phosphate group donor to produce nucleoside -5'-phosphate ester, and collecting it, wherein the microorganism is transformed with a recombinant DNA comprising a gene encoding an acid phosphate having an increased affinity for the nucleoside and/or an increased temperature affinity.

10 In another aspect, the present invention provides mutant acid phosphatases having an increased affinity for a nucleoside and/or an increased temperature stability, genes coding for the acid phosphatases, recombinant DNAs containing the genes, and microorganisms harboring the recombinant DNA.

Embodiments of the invention are described below by way of example only and with reference to the accompanying figures, of which:

15 Fig. 1 illustrates a relationship between reaction pH and produced amount of 5'-inosinic acid in a reaction performed by using an enzyme derived from Morganella morganii.

Fig. 2 illustrates a relationship between reaction pH and produced amount of 5'-inosinic acid in a reaction performed by using an enzyme derived from Escherichia blattae.

20 Fig. 3 illustrates a restriction enzyme map of a chromosomal DNA fragment of Morganella morganii containing a gene coding for an acid phosphatase.

Fig. 4 illustrates produced amount of 5'-inosinic acid in a reaction performed by using a strain harboring phosphatase gene derived from Morganella morganii.

Fig. 5 illustrates a restriction enzyme map of a chromosomal DNA fragment of Escherichia blattae containing a gene coding for an acid phosphatase.

25 Fig. 6 illustrates a diagram showing produced amount of 5'-inosinic acid in a reaction performed by using a strain harboring the acid phosphatase gene derived from Escherichia blattae.

Fig. 7 illustrates produced amount of 5'-inosinic acid in reactions performed by using a strain harboring the wild type acid phosphatase gene and a strain harboring the mutant acid phosphatase gene derived from Escherichia blattae respectively.

30 Fig. 8 illustrates produced amount of 5'-inosinic acid in a reaction performed by using a strain harboring the new mutant phosphatase gene derived from Escherichia blattae.

Fig. 9 illustrates a restriction enzyme map of a chromosomal DNA fragment derived from Enterobacter aerogenes which contains the gene coding for acid phosphatase.

35 Fig. 10 illustrates a restriction enzyme map of a chromosomal DNA fragment derived from Klebsiella planticola which contains the gene coding for acid phosphatase.

Fig. 11 illustrates a restriction enzyme map of a chromosomal DNA fragment derived from Serratia ficaria which contains the gene coding for acid phosphatase.

40 Fig. 12 illustrates amino acid sequences in one-letter deduced from nucleotide sequences of acid phosphatases derived from Morganella morganii, Escherichia blattae, Providencia stuartii, Enterobacter aerogenes, Klebsiella planticola and Serratia ficaria. These amino acid sequences are illustrated in SEQ ID NOs: 4, 8, 22, 24, 26 and 28 in Sequence Listing in three-letter. In the figure, the amino acid residues which is common through the all amino acid sequences are marked with * below the sequence.

Fig. 13 illustrates the graph of the temperature stability of the acid phosphatase activity in the cell free extract solution prepared from a strain harboring the new mutant phosphatase gene derived from Escherichia blattae.

<1> Preparation of acid phosphatase

The acid phosphatase to be used in the present invention is not specifically limited provided that it catalyzes the reaction to produce nucleoside-5'-phosphate ester by phosphate group transfer to the nucleoside from the phosphate group donor, for example, selected from the group consisting of polyphosphoric acid or a salt thereof, phenylphosphoric acid or a salt thereof, acethylphosphoric acid or a salt, and carbamyl phosphate or a salt thereof under the condition of pH 3.0 to 5.5. Such an acid phosphatase preferably includes those derived from microorganisms. In an especially preferred embodiment, the present invention uses an enzyme derived from a bacterium belonging to the genus Morganella, Escherichia, Providencia,

55 Enterobacter, Klebsiella or Serratia. Representative examples of such a bacterium include the following bacterial strains.

Morganella morganii NCIMB 10466

Morganella morganii IFO 3168
Morganella morganii IFO 3848
Escherichia blattae JCM 1650
Escherichia blattae ATCC 33429
Escherichia blattae ATCC 33430
Providencia stuartii ATCC 29851
Providencia stuartii ATCC 33672
Enterobacter aerogenes IFO 12010
Enterobacter aerogenes IFO 13534
Klebsiella planticola IFO 14939
Klebsiella planticola IAM 1133
Serratia ficaria IAM 13540
Serratia marcescens IAM 12143

It is noted that acid phosphatase (EC 3.1.3.2) is originally an enzyme which catalyzes a reaction to hydrolyze phosphate ester under an acidic condition, and it has a nucleotidase activity to degrade nucleoside-5'-phosphate ester produced by the transphosphorylation reaction (hereinafter, the nucleotidase activity is referred to as "phosphomonoesterase activity"). Even such an acid phosphatase can be used in the method for producing nucleoside-5'-phosphate ester of the present invention. However, in order to obtain nucleoside-5'-phosphate ester at a high yield, it is desirable to use the mutant acid phosphatase in which an affinity for a nucleoside in the transphosphorylation reaction onto the nucleoside is increased as compared with the wild type acid phosphatase produced by the bacteria as described above (hereinafter simply referred to as "mutant acid phosphatase", if necessary). Preferably the mutant acid phosphatase having a K_m value below 100 is used.

The mutant acid phosphatase may be obtained by expressing a mutant gene obtained by directly mutating a gene coding for an acid phosphatase as described below. Alternatively, the mutant acid phosphatase may be also obtained by treating a microorganism which produces an acid phosphatase with irradiation of ultraviolet light or a mutating agent usually used for artificial mutation such as N-methyl-N'-nitro-N-nitrosoguanidine (NTG), and cultivating a microorganism mutated to produce a mutant acid phosphatase having an increased affinity for a nucleoside and/or an increased temperature stability.

A protein having the acid phosphatase activity may be obtained from the microorganisms as described above by cultivating the microbial strain having the activity in an appropriate medium, harvesting proliferated microbial cells, disrupting the microbial cells to prepare a cell-free extract, and adequately purifying the protein therefrom.

The medium for cultivating the microorganism is not specifically limited, for which an ordinary medium may be available, containing an ordinary carbon source, a nitrogen source, inorganic ions, and optionally an organic nutrient source. The carbon source to be adequately used includes, for example, saccharides such as glucose and sucrose, alcohols such as glycerol, and organic acids. The nitrogen source to be used includes, for example, ammonia gas, aqueous ammonia, and ammonium salts. The inorganic ions to be adequately used if necessary include, for example, magnesium ion, phosphate ion, potassium ion, iron ion, and manganese ion. The organic nutrient source to be adequately used includes, for example, vitamins and amino acids as well as those containing them such as yeast extract, peptone, meat extract, corn steep liquor, casein hydrolysate, and soybean hydrolysate.

The cultivation condition is also not specifically limited. The microorganism may be cultivated, for example, under an aerobic condition for about 12 to 48 hours while appropriately controlling pH and temperature within ranges of pH 5 to 8 and temperature of 25 to 40 °C.

Proliferated microbial cells may be harvested from a culture liquid, for example, by centrifugation. The cell-free extract is prepared from the harvested microbial cells by using an ordinary method. Namely, the cell-free extract is obtained by disrupting the microbial cells by means of a method such as ultrasonic treatment, Dyno-mill, and French Press, and removing cell debris by centrifugation.

The acid phosphatase is purified from the cell-free extract by using an adequate combination of techniques usually used for enzyme purification such as ammonium sulfate fractionation, ion exchange chromatography, hydrophobic chromatography, affinity chromatography, gel filtration chromatography, and isoelectric purification. As for the precipitation, it is not necessarily indispensable to completely purify the acid phosphatase. It is sufficient to achieve removal of contaminants such as an enzyme which participates in degradation of nucleoside as the substrate.

<2> Preparation of acid phosphatase gene

A DNA fragment, which contains a structural gene coding for the protein having the acid phosphatase activity, can be cloned starting from, for example, cells of the microorganism having the enzyme activity. The cloning method includes, for example, a method in which a chromosomal gene expression library is screened by using the enzyme

activity as an index, a method in which an antibody against the protein is prepared to screen a chromosomal gene expression library, and a method in which an amino acid sequence such as an N-terminal sequence of the purified protein is analyzed, on the basis of which a probe is prepared to screen a gene library.

Specifically, the gene coding for the acid phosphatase of Morganella morganii, Escherichia blattae, Providencia stuartii, Enterobacter aerogenes, Klebsiella planticola, Serratia ficaria or Serratia marcescens described above can be cloned by preparing a chromosomal gene expression library of each of the microorganisms, and screening the library by using the phosphatase activity as an index.

Namely, a chromosomal gene expression library can be prepared by firstly preparing chromosomal DNA from Morganella morganii or Escherichia blattae, partially degrading it with an appropriate restriction enzyme, subsequently ligating it with a vector autonomously replicable in Escherichia coli, and transforming Escherichia coli with the obtained recombinant DNA. A wide variety of restriction enzymes can be used for digesting chromosomal DNA by adjusting the digestion reaction time to adjust the degree of digestion. Any vector may be used for cloning the gene provided that it is autonomously replicable in Escherichia coli. It is possible to use, for example, pUC19, pUC118, pHSG298, pBR322, and pBluescript II.

The vector may be ligated with the DNA fragment containing the gene coding for the acid phosphatase to prepare the recombinant DNA by previously digesting the vector with the same restriction enzyme as that used for digesting chromosomal DNA, or with a restriction enzyme which generates a cleaved edge complementary with a cleaved edge of the chromosomal DNA fragment, and ligating it with the DNA fragment by using ligase such as T4 DNA ligase. Any microbial strain may be used as a recipient for the prepared recombinant DNA provided that it is appropriate for replication of the vector. It is possible to use, for example, microbial strains of Escherichia coli such as HB101, JM109, and DH5.

Transformants thus obtained are grown on an agar medium to form their colonies. After that, when a reaction solution containing p-nitrophenylphosphoric acid is poured onto a surface of the medium to perform a reaction, then a strain, which has expressed the phosphatase activity, liberates p-nitrophenol and exhibits a yellow color. A transformant, which harbors a DNA fragment containing the gene coding for the objective acid phosphatase, can be selected by performing the reaction described above under an acidic condition, and selecting the transformant by using the color development as an index.

After that, a recombinant DNA is recovered from the selected transformant to analyze the structure of the DNA fragment containing the gene coding for the acid phosphatase ligated with the vector. A nucleotide sequence of the gene coding for the acid phosphatase is shown in SEQ ID NO: 2 in Sequence Listing in the case of a gene derived from Morganella morganii NCIMB 10466, SEQ ID NO: 6 in Sequence Listing in the case of a gene derived from Escherichia blattae JCM 1650, SEQ ID NO: 21 in Sequence Listing in the case of a gene derived from Providencia stuartii ATCC 29851, SEQ ID NO: 23 in Sequence Listing in the case of a gene derived from Enterobacter aerogenes IFO 12010, SEQ ID NO: 25 in Sequence Listing in the case of a gene derived from Klebsiella planticola IFO14939, or SEQ ID NO: 27 in Sequence Listing in the case of a gene derived from Serratia ficaria IAM 13540.

The deduced amino acid sequences of the acid phosphatases encoded by the above genes are illustrated in SEQ ID NO: 4, 8, 22, 24, 26 and 28.

Variants of the acid phosphatases encoded by the above genes and having increased affinity for nucleoside and/or increased temperature stability, are preferably used for the present invention. Acid phosphatase comprising an amino acid sequence which is substantially identical with an amino acid sequence of any one of the acid phosphatases encoded by the above genes is also preferably used for the present invention. The term "substantially identical" means that amino acid sequences of the acid phosphatases may have substitution, deletion, insertion or transition of one or a plurality of amino acid residues without losing an activity to produce nucleoside-5'-phosphate ester (hereinafter referred to as "transphosphorylation activity"). Preferably, the variants have a Michaelis constant K_m below 100°C as discussed above and experience substantially no loss of activity when held at 50°C and pH7 for 30 minutes.

<3> Preparation of gene coding for mutant acid phosphatase

The wild type acid phosphatase obtained as described above has a phosphomonoesterase activity. Therefore, the phosphomonoesterase activity may serve as a factor to cause accompanying degradation of the product as the reaction time passes in the production of nucleoside-5'-phosphate ester, resulting in decrease in reaction yield. In order to overcome such a circumstance, it is advantageous to cause artificial mutation on the gene coding for the acid phosphatase so that an affinity for a nucleoside is increased.

Further conducting a phosphate transfer reaction by the acid phosphatase at a higher temperature leads to a much more effective production of nucleoside-5'-phosphate because the reaction speed is elevated and the concentration of a phosphate receiver in the reaction solution can be higher. For the purpose it is advantageous to cause artificial mutation on the gene coding for the acid phosphatase so that a temperature stability is increased.

Methods for site-directed mutagenesis for causing objective mutation at an objective site of DNA include, for ex-

ample, a method using PCR (Higuchi, R., 61, in PCR technology, Erlich, H. A. Eds., Stockton press (1989); carter, P., Meth. in Enzymol., 154, 382 (1987)), and a method using phage (Kramer, W. and Frits, H. J., Meth. in Enzymol., 154, 350 (1987); Kunkel, T. A. et al., Meth. in Enzymol., 154, 367 (1987)).

The mutant acid phosphatase having the increased affinity for the nucleoside is exemplified by the acid phosphatase comprising an amino acid sequence which is substantially identical with an amino acid sequence selected from the group consisting of sequences illustrated in SEQ ID NOs: 4, 8, 22, 24, 26 and 28 in Sequence Listing, and has mutation which increases the affinity for the nucleoside compared to the wild type acid phosphatase. Concretely, the mutant acid phosphatase is exemplified, for the enzyme derived from Escherichia blattae JCM 1650, by one in which the 74th glycine residue and/or the 153th isoleucine residue is substituted with another amino acid residue in an amino acid sequence illustrated in SEQ ID NO: 8 in Sequence Listing. In Examples described below, a gene coding for mutant acid phosphatase is illustrated as an example in which the 74th glycine residue is substituted with an aspartic acid residue, and the 153th isoleucine residue is substituted with a threonine residue.

Further mutations selected from the group consisting of substitutions of the 63rd leucine residue, the 65th alanine residue, the 66th glutamic acid residue, the 69th aspartic acid residue, the 71st serine residue, the 72nd serine residue, the 85th serine residue, the 92nd alanine residue, the 94th alanine residue, the 116th aspartic acid residue, the 130th serine residue, the 135th threonine residue and/or the 136th glutamic acid residue with another amino acid in SEQ ID NO: 8 in Sequence Listing further increase the affinity for the nucleoside of the acid phosphatase.

The mutant acid phosphatase having the increased temperature stability is exemplified by the acid phosphatase comprising an amino acid sequence which is substantially identical with an amino acid sequence selected from the group consisting of sequences illustrated in SEQ ID NOs: 4, 8, 22, 24, 26 and 28 in Sequence Listing, and has mutation which increases the temperature stability of wild type acid phosphatase. Concretely, the mutant acid phosphatase is exemplified, for the enzyme derived from Escherichia blattae JCM 1650, by one in which the 104th glutamic acid residue and/or the 151st threonine residue is substituted with another amino acid residue in an amino acid sequence illustrated in SEQ ID NO: 8 in Sequence Listing. In Examples described below, a gene coding for mutant acid phosphatase is illustrated as an example in which the 104th glutamic acid residue is substituted with a glycine residue, and the 151st threonine residue is substituted with an alanine residue.

Therefore, the nucleotide may be substituted at the specified site of the wild type gene in accordance with the site-directed mutagenesis method described above so that these mutant acid phosphatases are encoded. The mutation to increase the affinity for the nucleoside is desirably a type of mutation by which the activity to produce nucleoside-5'-phosphate ester is not substantially lowered in comparison with wild type acid phosphatase. However, even in the case that the activity to produce nucleoside-5'-phosphate ester is lowered, it will be sufficient if degree of decrease of phosphomonoesterase activity is larger than that of the activity to produce nucleoside-5'-phosphate ester, with the result that a ratio of phosphomonoesterase activity to the activity to produce nucleoside-5'-phosphate ester of the mutant acid phosphatase is lowered in comparison with the wild type acid phosphatase. As for the degree of increase in the affinity for the nucleoside, the K_m value to the nucleoside in the transphosphorylation reaction is preferably below 100.

The mutation which increases the temperature stability means one which has more residual activity after a temperature treatment than the wild type acid phosphatase has. The degree of the temperature stability increase is preferably the one that does not cause the decrease in an activity with the treatment at pH 7.0, 50°C, 30 minutes.

As illustrated below in the embodiments, the amino acid sequence of the acid phosphatase of Escherichia blattae JCM 1650 is highly homologous to that of Morganella morganii NCIMB 10466, and the 72nd glycine residue, the 102th glutamic acid residue, the 149th threonine residue and the 151th isoleucine residue in an amino acid sequence illustrated in SEQ ID NO: 4 correspond to the 74th glycine residue, the 104th glutamic acid residue, the 151st threonine residue and the 153rd isoleucine residue in an amino acid sequence illustrated in SEQ ID NO: 8 respectively. Further, in addition to Escherichia blattae JCM 1650, amino acid sequences of acid phosphatases derived from microorganisms such as Providencia stuartii ATCC 29851, Enterobacter aerogenes IFO 12010, Klebsiella planticola IFO 14939, and Serratia ficaria IAM 13450 have high homology with that of Morganella morganii NCIMB 10466, and amino acid sequences of these acid phosphatases include amino acids residues each of which corresponds to the 72nd glycine residue, the 102nd glutamic acid residue, the 149th threonine residue and the 151st isoleucine residue in an amino acid sequence illustrated in SEQ ID NO: 4 respectively. Therefore, genes coding for mutant acid phosphatases derived from these microorganisms may be obtained as described above. The 92nd glycine residue, the 122nd glutamic acid residue, the 169th threonine residue and the 171st isoleucine residue in the amino acid sequence of the acid phosphatase derived from Providencia stuartii ATCC 29851, Enterobacter aerogenes IFO 12010 or Klebsiella planticola IFO 14939 illustrated in SEQ ID NO: 22, 24 or 26, and the 88th glycine residue, the 118th glutamic acid residue, the 165th threonine residue and the 167th isoleucine residue in the amino acid sequence of the acid phosphatase derived from Serratia ficaria IAM 13450 illustrated in SEQ ID NO: 28 respectively correspond to the 72nd glycine residue, the 102nd glutamic acid residue, the 149th threonine residue and the 151st isoleucine residue in an amino acid sequence illustrated in SEQ ID NO: 4.

The result of comparing the amino acid sequences of the above acid phosphatase is illustrated in Fig. 12. Based on Fig. 12, it is decided which amino acid residue of one acid phosphatase corresponds to another amino acid residue of another acid phosphatase.

5 <4> Introduction of acid phosphatase gene into host

A recombinant microorganism for expressing the acid phosphatase activity at a high level can be obtained by introducing the DNA fragment containing the gene coding for the protein having the acid phosphatase activity obtained as described above into cells of a host after recombining the DNA fragment again with an appropriate vector. In such a procedure, the wild type acid phosphatase is expressed by using the gene coding for the wild type acid phosphatase, while the mutant acid phosphatase is expressed by using the gene coding for the mutant acid phosphatase.

The host includes the microbial strains of *Escherichia coli* such as HB101, JM109, and DH5 described above. Other than these strains, all bacteria can be utilized as the host provided that a replication origin of constructed recombinant DNA and the acid phosphatase gene make their functions, the recombinant DNA is replicable, and the acid phosphatase gene is expressible. One of the most preferred hosts is *Escherichia coli* JM109.

The vector for incorporating the gene coding for the acid phosphatase thereinto is not specifically limited provided that it is replicable in the host. When *Escherichia coli* is used as the host, the vector may be exemplified by plasmids autonomously replicable in this bacterium. For example, it is possible to use ColE1 type plasmids, p15A type plasmids, R factor type plasmids, and phage type plasmids. Such plasmids specifically include, for example, pBR322 (Gene, 2, 95 (1977)), pUC19 (Gene, 33, 103 (1985)), pUC119 (Methods in Enzymology, 153, 3 (1987)), pACYC184 (J. Bacteriol., 134, 1141 (1978)), and pSC101 (Proc. Natl. Acad. Sci. U.S.A., 70, 3240 (1973)).

When the DNA fragment containing the gene coding for the acid phosphatase contains a promoter which is functional in the host, the DNA fragment may be ligated with the vector as it is. When the DNA fragment does not contain such a promoter, another promoter which works in the host microorganism such as lac, trp, and PL may be ligated at a position upstream from the gene. Even when the DNA fragment contains the promoter, the promoter may be substituted with another promoter in order to efficiently express the gene coding for the acid phosphatase.

There is no special limitation for a method for introducing, into the host, the recombinant DNA constructed by ligating the vector with the DNA fragment containing the gene coding for the acid phosphatase. The recombinant DNA may be introduced into the host by using an ordinary method. When *Escherichia coli* is used as the host, it is possible to use, for example, a calcium chloride method (J. Mol. Biol., 53, 159 (1970)), a method of Hanahan (J. Mol. Biol., 166, 557 (1983)), an SEM method (Gene, 96, 23 (1990)), a method of Chung et al. (Proc. Natl. Acad. Sci. U.S.A., 86, 2172 (1989)), and electroporation (Nucleic Acids Res., 16, 6127 (1988)).

The acid phosphatase gene may be inserted into the autonomously replicable vector DNA, which may be introduced into the host so that it is harbored by the host as extrachromosomal DNA as described above. Alternatively, the acid phosphatase gene may be incorporated into chromosome of the host microorganism in accordance with a method which uses transduction, transposon (Biotechnol., 1, 417 (1983)), Mu phage (Japanese Patent Laid-open No. 2-109985), or homologous recombination (Experiments in Molecular Genetics, Cold Spring Harbor Lab. (1972)).

40 <5> Expression of acid phosphatase gene by recombinant microorganism

The transformant obtained as described above, into which the recombinant DNA containing the gene coding for the acid phosphatase has been introduced, is capable of expressing the acid phosphatase activity at a high level in its cells by cultivating it in an appropriate medium containing a carbon source, a nitrogen source, inorganic ions, and optionally an organic nutrient source. The carbon source to be adequately used includes, for example, carbohydrates such as glucose, alcohols such as glycerol, and organic acids. The nitrogen source to be used includes, for example, ammonia gas, aqueous ammonia, and ammonium salts. The inorganic ions to be adequately used if necessary include, for example, magnesium ion, phosphate ion, potassium ion, iron ion, and manganese ion. The organic nutrient source to be adequately used includes, for example, vitamins and amino acids as well as those containing them such as yeast extract, peptone, meat extract, corn steep liquor, casein hydrolysate, and soybean hydrolysate. The amount of expression of the acid phosphatase activity may be increased by adding, to the medium, an expression-inducing agent depending on a promoter such as IPTG (isopropyl- β -D-thiogalactopyranoside).

The cultivation condition is also not specifically limited. The cultivation may be performed, for example, under an aerobic condition for about 12 to 48 hours while appropriately controlling pH and temperature within ranges of pH 5 to 8 and temperature of 25 to 40 °C.

After that, microbial cells are harvested from a culture, and a cell-free extract is obtained by disruption, from which the acid phosphatase can be purified. The purification is performed by using an appropriate combination of techniques usually used for enzyme purification such as those described in the aforementioned item <1>. As for the purification, it is not necessarily indispensable to completely purify the acid phosphatase. It is sufficient to achieve removal of

contaminants such as an enzyme which participates in degradation of nucleoside as the substrate.

<6> Production of nucleoside-5'-phosphate ester

Nucleoside-5'-phosphate ester can be produced in a reaction mixture by allowing the acid phosphatase obtained as described above, and having increased affinity for nucleoside and/or increased temperature stability, such as the mutant acid phosphatase obtained by expressing the gene in a large amount in accordance with the genetic engineering technique as described in the item <5> to make contact and cause the reaction of a nucleoside with a phosphate group donor selected from the group consisting of polyphosphoric acid or a salt thereof, phenylphosphoric acid or a salt thereof, acetylphosphoric acid or a salt thereof, and carbamyl phosphate or a salt thereof. In order to achieve a high productivity in this reaction, it is important to adjust pH of the reaction solution to be weakly acidic in a range of 3.0 to 5.5.

When the gene coding for the acid phosphatase is expressed in a large amount by means of the genetic engineering technique, especially when the gene coding for the mutant acid phosphatase having the increased affinity for the nucleoside is expressed in a large amount, then it is also possible to produce nucleoside-5'-phosphate ester inexpensively and efficiently by using a culture containing microbial cells of the transformant, the microbial cells separated and harvested from the culture, or a product obtained from the microbial cells in accordance with, for example, an immobilizing treatment, an acetone treatment, or a lyophilizing treatment, instead of the purified acid phosphatase.

The nucleoside to be used includes, for example, purine nucleosides such as inosine, guanosine, adenosine, xanthosine, purine riboside, 6-methoxypurine riboside, 2,6-diaminopurine riboside, 6-fluoropurine riboside, 6-thiopurine riboside, 2-amino-6-thiopurine riboside, and mercaptoguanosine; and pyrimidine nucleosides such as uridine, cytidine, 5-aminouridine, 5-hydroxyuridine, 5-bromouridine, and 6-azauridine. As a result of the reaction, these natural type nucleosides and nonnatural type nucleosides are specifically phosphorylated at their 5'-positions, and corresponding nucleoside-5'-phosphate esters are produced respectively.

The nucleoside is desirably added to the reaction solution at a concentration of 1 to 20 g/dl. In the case of use of a nucleoside which is scarcely soluble in water, the reaction yield may be improved by adding boric acid or a surfactant such as dimethyl sulfoxide.

When the nucleoside is produced by fermentation, the fermentation medium after the fermentation as such can be added to the phosphorylation reaction liquid. When an element decomposing the nucleoside-5'-phosphate ester is included in the medium, a purification step is preferably employed so that said element is removed.

As for the phosphate group donor to be used, those usable as the polyphosphoric acid or the salt thereof include, for example, pyrophosphoric acid, tripolyphosphoric acid, trimetaphosphoric acid, tetrametaphosphoric acid, hexametaphosphoric acid, mixtures thereof, sodium salts thereof, potassium salts thereof, and mixtures of these salts. Those usable as the phenylphosphoric acid or the salt thereof include, for example, disodium phenylphosphate, dipotassium phenylphosphate, O,O-diphenylphosphoric acid anhydride, and mixtures thereof. Those usable as the carbamyl phosphate or the salt thereof include, for example, disodium carbamyl phosphate, dipotassium carbamyl phosphate, diammonium carbamyl phosphate, dilithium carbamyl phosphate, and mixtures thereof. Those usable as the acetylphosphoric acid or the salt thereof include, for example, lithium potassium acetylphosphate. The concentration at which the phosphate group donor is used is determined by the concentration of the nucleoside as the phosphate group acceptor. The phosphate group donor is usually used in an amount which is 1 to 5 times that of the nucleoside.

A preferred result is obtained in the reaction usually at a temperature of 20 to 60 °C, preferably 30 to 40 °C at a pH on a weakly acidic side of 3.5 to 6.5, preferably 4.0 to 5.0. A reaction temperature when using the mutant acid phosphatase with an increased temperature stability is 20 to 70 °C, preferably 30 to 60 °C. The reaction may be performed by adopting any one of a stationary method and an agitating method. The reaction time defers depending on the condition such as the activity of the enzyme to be used and the substrate concentration, however, it is 1 to 100 hours.

The nucleoside-5'-phosphate ester thus produced may be collected and separated from a mixture after completion of the reaction by adopting a method to use a synthetic resin for adsorption, a method to use a precipitating agent, and other ordinary methods for collection and separation.

[EXAMPLE]

Embodiments of the present invention will be specifically explained below with reference to Examples, however, the present invention is not limited to these Examples.

The transphosphorylation activity was measured under the following condition using inosine as a substrate. The reaction was performed at pH 5.0 at 30 °C for 10 minutes in a reaction solution (1 ml) containing 40 µmol/ml of inosine, 100 µmol/ml of sodium pyrophosphate, 100 µmol/ml of sodium acetate buffer (pH 5.0), and an enzyme. The reaction was stopped by adding 200 µl of 2 N hydrochloric acid. After that, precipitates were removed by centrifugation. Then, 5'-Inosinic acid produced by the transphosphorylation reaction was quantitatively measured. An amount of enzyme to

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produce 1 μmol of 5'-inosinic acid per 1 minute under this standard reaction condition was defined as 1 unit.

The phosphomonoesterase activity was measured under the following condition using 5'-inosinic acid as a substrate. The reaction was performed at 30 °C for 10 minutes in a reaction solution (1 ml) containing 10 $\mu\text{mol}/\text{ml}$ of 5'-inosinic acid, 100 $\mu\text{mol}/\text{ml}$ of MES/NaOH buffer (pH 6.0), and an enzyme. The reaction was stopped by adding 200 μl of 2 N hydrochloric acid. After that, precipitates were removed by centrifugation. Then, inosine produced by the hydrolytic reaction was quantitatively measured. An amount of enzyme to produce 1 μmol of inosine per 1 minute under this standard reaction condition was defined as 1 unit.

Inosine and 5'-inosinic acid were analyzed under the following condition by means of high-performance liquid chromatography (HPLC).

Column: Cosmosil 5C18-AR (4.6 x 150 mm) [produced by nacalai tesque];
Mobile phase: 5 mM potassium phosphate buffer (pH 2.8)/methanol = 95/5;
Flow rate: 1.0 ml/min;
Temperature: room temperature;
Detection: UV 245 nm.

Incidentally, in the reaction to produce nucleoside-5'-phosphate esters using nucleosides other than inosine as raw materials, the nucleosides as raw materials and produced nucleoside-5'-phosphate esters were analyzed by HPLC as described above.

Example 1: Purification and Characterization of Acid Phosphatase Derived from *Morganella morganii*

A nutrient medium (pH 7.0, 50 ml) containing 1 g/dl of peptone, 0.5 g/dl of yeast extract, and 1 g/dl of sodium chloride was poured into Sakaguchi flasks (500 ml), which was sterilized at 120 °C for 20 minutes. A slant culture of *Morganella morganii* NCIMB 10466 was inoculated to each of the flasks once with a platinum loop, which was cultivated at 30 °C for 16 hours with shaking. Microbial cells (about 3,000 g), which were harvested from a culture by centrifugation, were suspended in 100 mM potassium phosphate buffer (1 L, pH 7.0). A ultrasonic treatment was performed at 4 °C for 20 minutes to disrupt the microbial cells. The treated suspension was centrifuged to remove its insoluble fraction. Thus a cell-free extract was prepared.

Ammonium sulfate was added to the cell-free extract so that 30 % saturation was achieved. Appeared precipitate was removed by centrifugation, and then ammonium sulfate was further added to supernatant so that 60 % saturation was achieved. Appeared precipitate was collected by centrifugation, and it was dissolved in 100 mM potassium phosphate buffer.

This crude enzyme solution was dialyzed four times against 5 L of 100 mM potassium phosphate buffer (pH 7.0), and then it was applied to a DEAE-Toyopeal 650M column (ϕ 4.1 x 22 cm) equilibrated with 20 mM potassium phosphate buffer (pH 7.0), followed by washing with 800 ml of 20 mM potassium phosphate buffer (pH 7.0). The transphosphorylation activity was found in a fraction which passed through the column, and thus the fraction was recovered.

The fraction was added with ammonium sulfate so that 35 % saturation was achieved, which was adsorbed to a Butyl-Toyopeal column (ϕ 3.1 x 26 cm) equilibrated with 20 mM potassium phosphate buffer (pH 7.0) containing ammonium sulfate at 35 % saturation. Elution was performed by using a linear concentration gradient from 35 % saturation to 20 % saturation in potassium phosphate buffer (pH 7.0).

Active fractions were collected and dialyzed against 1 L of 50 mM potassium phosphate buffer (pH 7.0), followed by being applied to a hydroxyapatite column (ϕ 5 x 6.5 cm) equilibrated with 50 mM potassium phosphate buffer (pH 7.0). Elution was performed by using a linear concentration gradient from 50 mM to 300 mM of potassium phosphate buffer (pH 7.0).

Active fractions were collected and concentrated by ultrafiltration. This enzyme solution was applied into a HiLoad TM 16/60 Superdex 200 column (produced by Pharmacia). Elution was performed at a flow rate of 1.0 ml/minute by using 50 mM potassium phosphate buffer containing 100 mM sodium chloride.

In accordance with the procedure as described above, the enzyme exhibiting the transphosphorylation activity was purified from the cell-free extract consequently about 550-fold at a recovery ratio of about 10 %. The specific activity and the recovery ratio in this purification process are shown in Table 1. This enzyme sample was homogeneous on SDS-polyacrylamide gel electrophoresis.

Table 1

Step Recovery	Total activity (unit)	Total protein (mg)	Specific activity (unit/mg)	ratio (%)
1. Cell-free extract	597	127,200	0.005	100

Table 1 (continued)

Step Recovery	Total activity (unit)	Total protein (mg)	Specific activity (unit/mg)	ratio (%)
2. Ammonium sulfate fractionation (30 to 60 %)	568	122,210	0.005	95
3. DEAE-Toyopearl	517	36,498	0.014	87
4. Butyl-Toyopearl	394	1,121	0.351	66
5. Hydroxyapatite	112	50	2.244	19
6. Superdex 200	63	24	2.630	10

The purified enzyme had the following properties.

(1) Action: Phosphate group is transferred from a phosphate group donor such as polyphosphoric acid to nucleoside, and nucleoside-5'-phosphate ester is produced. Reversely, this enzyme also exhibits an activity to hydrolyze phosphate ester.

(2) Substrate specificity: Those which serve as the phosphate group donor in the transphosphorylation reaction include, for example, pyrophosphoric acid, tripolyphosphoric acid, trimetaphosphoric acid, tetrametaphosphoric acid, hexametaphosphoric acid, disodium phenylphosphate, dipotassium phenylphosphate, O,O-diphenylphosphoric acid anhydride, disodium carbamyl phosphate, dipotassium carbamyl phosphate, diammonium carbamyl phosphate, and dilithium carbamyl phosphate. Those which serve as the phosphate group acceptor include, for example, purine riboside, inosine, guanosine, adenosine, xanthosine, uridine, and cytidine. On the other hand, those which undergo the action in the phosphate ester hydrolytic reaction include, for example, inorganic phosphoric acid such as pyrophosphoric acid, tripolyphosphoric acid, trimetaphosphoric acid, tetrametaphosphoric acid, hexametaphosphoric acid; phosphate ester such as disodium phenylphosphate, dipotassium phenylphosphate, O,O-diphenylphosphoric acid anhydride, disodium carbamyl phosphate, dipotassium carbamyl phosphate, diammonium carbamyl phosphate, and dilithium carbamyl phosphate; and 5'-nucleotide such as 5'-purine ribotide, 5'-inosinic acid, 5'-guanylic acid, 5'-adenylic acid, 5'-xanthylic acid, 5'-uridylic acid, and 5'-cytidylic acid.

(3) Optimum pH: 5.2 (transphosphorylation reaction), 6.5 (phosphate ester hydrolytic reaction).

(4) pH stability: pH 3.0 to 12.0 (treatment at 30 °C for 60 minutes).

(5) Optimum temperature: about 35 °C.

(6) Temperature stability: stable up to 30 °C (treatment at pH 7.0 for 30 minutes).

(7) Effect of the addition of metal ion and inhibitor: This enzyme exhibits no activation phenomenon relevant to its activity by addition of any metal ion. The activity is inhibited by Ag²⁺, Pb²⁺, Hg²⁺, and Cu²⁺. The activity is also inhibited by iodoacetic acid.

(8) Molecular weight: A calculated molecular weight is about 190,000 in accordance with high-performance liquid chromatography (TSKgel G-3000SW, produced by Toyo Soda).

(9) Subunit molecular weight: A calculated subunit molecular weight is about 25,000 in accordance with SDS-polyacrylamide gel electrophoresis.

This enzyme exhibits not only the activity to transfer phosphate group to nucleoside, but also the activity to reversely hydrolyze phosphate ester. Moreover, this enzyme exhibits the phosphate ester hydrolytic activity (phosphomonoesterase activity) which is higher than the transphosphorylation activity by not less than 20 times. Other properties are well coincident with those of a known acid phosphatase produced by a bacterium belonging to the genus *Morganella* (*Microbiology*, 140, 1341-1350 (1994)). Accordingly, it has been clarified that this enzyme is an acid phosphatase.

Sodium pyrophosphate (10 g/dl) and inosine (2 g/dl) were dissolved in sodium acetate buffers each having pH of 5.5, 5.0, 4.5, 4.0, and 3.5, to which the enzyme sample described above was added so that a concentration of 50 units/dl was obtained. The reaction mixture was incubated at 30 °C for 6 hours while maintaining each pH, and the amount of produced 5'-inosinic acid was measured along with passage of time. Produced inosinic acid contained only 5'-inosinic acid. By-production of 2'-inosinic acid and 3'-inosinic acid was not observed at all. A result is shown in Fig. 1. The velocity of 5'-inosinic acid production was maximum at pH 5.0. However, the maximum accumulated amount of 5'-inosinic acid was higher at lower pH. The reaction condition at pH 4.0 was most efficient for production of 5'-inosinic acid, in which 5'-inosinic acid was produced and accumulated in an amount of 2.60 g/dl by performing the reaction for 3 hours.

Example 2: Phosphorylation Reaction of Various Nucleosides by Acid Phosphatase Sample Derived from *Morganella morganii*

Sodium pyrophosphate (10 g/dl) and inosine, guanosine, uridine, or cytidine (2 g/dl) as a phosphate group acceptor were dissolved in sodium acetate buffer (pH 4.0), to which the enzyme sample prepared in Example 1 was added so that its concentration was 50 units/dl. The reaction mixture was incubated at 30 °C for 3 hours while maintaining pH at 4.0. The amount of nucleoside-5'-ester produced by the reaction is shown in Table 2.

Produced nucleotide contained only nucleoside-5'-ester. By-production of nucleoside-2'-ester and nucleoside-3'-ester was not observed at all.

Table 2

Nucleoside	Product	Produced amount (g/dl)
Inosine	5'-inosinic acid	2.60
Guanosine	5'-guanylic acid	1.90
Uridine	5'-uridylic acid	1.30
Cytidine	5'-cytidylic acid	0.98

Example 3: Production of 5'-Inosinic acid from Various Phosphate Compounds as Phosphate Group Donors by Acid Phosphatase Sample Derived from *Morganella morganii*

Inosine (2 g/dl) and sodium tripolyphosphate, sodium polyphosphate (trade name: Polygon P, produced by Chiyoda Chemical), disodium phenylphosphate, or disodium carbamyl phosphate (10 g/dl) as a phosphate group donor were dissolved in sodium acetate buffer (pH 4.0), to which the enzyme sample prepared in Example 1 was added so that its concentration was 50 units/dl. The reaction mixture was incubated at 30 °C for 3 hours while maintaining pH at 4.0. The amount of 5'-inosinic acid produced by the reaction is shown in Table 3.

5'-Inosinic acid was efficiently produced and accumulated by using any of the phosphate group donors. However, the accumulated amount of 5'-inosinic acid was the highest when sodium polyphosphate was used as the phosphate group donor.

Table 3

Phosphate group donor	Produced 5'-inosinic acid (g/dl)
Sodium tripolyphosphate	2.10
Sodium polyphosphate	2.72
Disodium phenylphosphate	2.33
Disodium carbamyl phosphate	2.54

Example 4: Purification and Characterization of Acid Phosphatase Derived from *Escherichia blattae*

A nutrient medium (pH 7.0, 50 ml) containing 1 g/dl of peptone, 0.5 g/dl of yeast extract, and 1 g/dl of sodium chloride was poured into Sakaguchi flasks (500 ml), which was sterilized at 120 °C for 20 minutes. A slant culture of *Escherichia blattae* JCM 1650 was inoculated to each of the flasks once with a platinum loop, which was cultivated at 30 °C for 16 hours with shaking. Microbial cells were harvested from a culture by centrifugation. The microbial cells (about 3,300 g) were suspended in 100 mM potassium phosphate buffer (1 L, pH 7.0). A ultrasonic treatment was performed at 4 °C for 20 minutes to disrupt the microbial cells. The treated suspension was centrifuged to remove its insoluble fraction. Thus a cell-free extract was prepared.

Ammonium sulfate was added to the cell-free extract so that 30 % saturation was achieved. Appeared precipitate was removed by centrifugation, and then ammonium sulfate was further added to supernatant so that 60 % saturation was achieved. Appeared precipitate was recovered by centrifugation, and it was dissolved in 100 mM potassium phosphate buffer.

This crude enzyme solution was dialyzed four times against 5 L of 100 mM potassium phosphate buffer (pH 7.0), and then it was applied to a DEAE-Toyopeal 650M column (φ 6.2 x 35 cm) equilibrated with 20 mM potassium phosphate buffer (pH 7.0), followed by washing with 20 mM potassium phosphate buffer (pH 7.0). The transphosphorylation activity was found in a fraction which passed through the column, and thus the fraction was collected.

The active fraction was added with ammonium sulfate so that 35 % saturation was achieved, which was applied to a Butyl-Toyopeal column (φ 5.0 x 22.5 cm) equilibrated with 20 mM potassium phosphate buffer (pH 7.0) containing

ammonium sulfate at 35 % saturation. Elution was performed by using a linear concentration gradient from 35 % saturation to 20 % saturation in potassium phosphate buffer (pH 7.0).

Active fractions were collected and dialyzed against 1 L of 100 mM potassium phosphate buffer (pH 7.0), followed by being applied to a hydroxyapatite column (ϕ 3.0 x 7.0 cm) equilibrated with 100 mM potassium phosphate buffer (pH 7.0). Elution was performed by using a linear concentration gradient from 50 mM to 100 mM of potassium phosphate buffer (pH 7.0), and active fractions were collected.

This enzyme solution was dialyzed against 1 L of 10 mM potassium phosphate buffer (pH 6.0), followed by being applied to a CM-Toyopearl column (ϕ 2.0 x 14.0 cm) equilibrated with 10 mM potassium phosphate buffer (pH 6.0). Elution was performed by using a linear concentration gradient in potassium phosphate buffer (pH 6.0) containing from 0 mM to 300 mM potassium chloride. Active fractions eluted from the column were collected.

In accordance with the procedure as described above, the enzyme exhibiting the transphosphorylation activity was purified from the cell-free extract consequently about 600-fold at a recovery ratio of about 16 %. The specific activity and the recovery ratio in this purification process are shown in Table 4. This enzyme sample was homogeneous on SDS-polyacrylamide gel electrophoresis.

Table 4

Step	Total activity (unit)	Total protein (mg)	Specific activity (unit/mg)	Recovery ratio (%)
1. Cell-free extract	365	160,650	0.002	100
2. Ammonium sulfate fractionation (30 to 60 %)	340	138,895	0.002	93
3. DEAE-Toyopearl	318	30,440	0.010	87
4. Butyl-Toyopearl	232	661	0.347	63
5. Hydroxyapatite	96	96	1.000	26
6. CM-Toyopearl	59	43	1.365	16

The purified enzyme had the following properties.

(1) Action: Phosphate group is transferred from a phosphate group donor such as polyphosphoric acid to nucleoside, and nucleoside-5'-phosphate ester is produced. Reversely, this enzyme also exhibits an activity to hydrolyze phosphate ester.

(2) Substrate specificity: Those which serve as the phosphate group donor in the transphosphorylation reaction include, for example, pyrophosphoric acid, tripolyphosphoric acid, trimetaphosphoric acid, tetrametaphosphoric acid, hexametaphosphoric acid, disodium phenylphosphate, dipotassium phenylphosphate, O,O-diphenylphosphoric acid anhydride, disodium carbamyl phosphate, dipotassium carbamyl phosphate, diammonium carbamyl phosphate, and dilithium carbamyl phosphate. Those which serve as the phosphate group acceptor include, for example, purine riboside, inosine, guanosine, adenosine, xanthosine, uridine, and cytidine. On the other hand, those which undergo the action in the phosphate ester hydrolytic reaction include, for example, inorganic phosphoric acid such as pyrophosphoric acid, tripolyphosphoric acid, trimetaphosphoric acid, tetrametaphosphoric acid, hexametaphosphoric acid; phosphate ester such as disodium phenylphosphate, dipotassium phenylphosphate, O,O-diphenylphosphoric acid anhydride, disodium carbamyl phosphate, dipotassium carbamyl phosphate, diammonium carbamyl phosphate, and dilithium carbamyl phosphate; and 5'-nucleotide such as 5'-purine ribotide, 5'-inosinic acid, 5'-guanylic acid, 5'-adenylic acid, 5'-xanthylic acid, 5'-uridylic acid, and 5'-cytidylic acid.

(3) Optimum pH: 5.2 (transphosphorylation reaction), 6.5 (phosphate ester hydrolytic reaction).

(4) pH stability: pH 3.5 to 12.0 (treatment at 30 °C for 60 minutes).

(5) Optimum temperature: about 35 °C.

(6) Temperature stability: stable up to 40 °C (treatment at pH 7.0 for 30 minutes).

(7) Effect of the addition of metal ion and inhibitor: This enzyme exhibits no activation phenomenon relevant to its activity by addition of any metal ion. The activity is inhibited by Fe^{2+} , Ag^{2+} , Pb^{2+} , Hg^{2+} , and Cu^{2+} . The activity is also inhibited by iodoacetic acid.

(8) Molecular weight: A calculated molecular weight is about 188,000 in accordance with high-performance liquid chromatography (TSKgel G-3000SW, produced by Toyo Soda).

(9) Subunit molecular weight: A calculated subunit molecular weight is about 24,500 in accordance with SDS-polyacrylamide gel electrophoresis.

This enzyme also exhibits not only the activity to transfer phosphate group to nucleoside, but also the activity to

reversely hydrolyze phosphate ester, in the same manner as the enzyme purified from the cell-free extract of *Morganella morganii* NCIMB 10466. Moreover, this enzyme exhibits the phosphate ester hydrolytic activity (phosphomonoesterase activity) which is higher than the transphosphorylation activity by not less than 30 times. Accordingly, it has been clarified that this enzyme is an acid phosphatase.

Sodium pyrophosphate (15 g/dl) and inosine (3 g/dl) were dissolved in sodium acetate buffers each having pH of 5.5, 5.0, 4.5, 4.0, and 3.5, to which the enzyme sample described above was added so that a concentration of 50 units/dl was obtained. The reaction mixture was incubated at 30 °C for 6 hours while maintaining each pH, and the amount of produced 5'-inosinic acid was measured along with passage of time. Produced inosinic acid contained only 5'-inosinic acid. By-production of 2'-inosinic acid and 3'-inosinic acid was not observed at all. A result is shown in Fig. 2. The velocity of 5'-inosinic acid production was maximum at pH 5.0. However, the maximum accumulated amount of 5'-inosinic acid was higher at lower pH. The reaction condition at pH 4.0 was most efficient for production of 5'-inosinic acid. 5'-Inosinic acid was produced and accumulated in an amount of 1.56 g/dl by performing the reaction at 30 °C at pH 4.0 for 3 hours.

Example 5: Phosphorylation Reaction of Various Nucleosides by Acid Phosphatase Sample Derived from *Escherichia blattae*

Sodium pyrophosphate (15 g/dl) and inosine, guanosine, uridine, or cytidine (3 g/dl) were dissolved in sodium acetate buffer (pH 4.0), to which the enzyme sample prepared in Example 4 was added so that its concentration was 50 units/dl. The reaction mixture was incubated at 35 °C for 3 hours while maintaining pH at 4.0. The amount of produced nucleoside-5'-ester is shown in Table 5.

Produced nucleotide contained only nucleoside-5'-ester. By-production of nucleoside-2'-ester and nucleoside-3'-ester was not observed at all.

Table 5

Nucleoside	Product	Produced amount (g/dl)
Inosine	5'-inosinic acid	1.56
Guanosine	5'-guanylic acid	1.05
Uridine	5'-uridylic acid	1.87
Cytidine	5'-cytidylic acid	1.22

Example 6: Production of 5'-Inosinic acid from Various Phosphate Compounds as Phosphate Group Donors by Acid Phosphatase Sample Derived from *Escherichia blattae*

Inosine (2 g/dl) and sodium tripolyphosphate, sodium polyphosphate (trade name: Polygon P, produced by Chiyoda Chemical), disodium phenylphosphate, or disodium carbamyl phosphate (10 g/dl) as a phosphate group donor were dissolved in sodium acetate buffer (pH 4.0), to which the enzyme sample prepared in Example 4 was added so that its concentration was 50 units/dl. The reaction mixture was incubated at 35 °C for 3 hours while maintaining pH at 4.0. The amount of produced 5'-inosinic acid is shown in Table 6.

5'-Inosinic acid was efficiently produced and accumulated by using any of the phosphate group donors. However, the accumulated amount of 5'-inosinic acid was the highest when sodium polyphosphate was used as the phosphate group donor.

Table 6

Phosphate group donor	Produced 5'-inosinic acid (g/dl)
Sodium tripolyphosphate	1.20
Sodium polyphosphate	1.79
Disodium phenylphosphate	1.50
Disodium carbamyl phosphate	1.53

Example 7: Isolation of Gene Coding for Acid Phosphatase from Chromosome of *Morganella morganii*

(1) Determination of N-terminal amino acid sequence

The acid phosphatase purified from the cell-free extract of *Morganella morganii* NCIMB 10466 in accordance with

the method described in Example 1 was adsorbed to DITC membrane (produced by Milligen/Biosearch), and its N-terminal amino acid sequence was determined by using Prosequencer 6625 (produced by Milligen/Biosearch). An N-terminal amino acid sequence comprising 20 residues shown in SEQ ID NO: 1 in Sequence Listing was determined.

5 (2) Isolation of DNA fragment containing gene coding for acid phosphatase

Chromosomal DNA was extracted from cultivated microbial cells of *Morganella morganii* NCIMB 10466 in accordance with a method of Murray and Thomson (*Nucl. Acid Res.*, 4321, 8 (1980)). The chromosomal DNA was partially degraded with restriction enzyme *Sau3AI*. After that, DNA fragments of 3 to 6 kbp were fractionated by means of sucrose density gradient centrifugation. A plasmid vector pUC118 (produced by Takara Shuzo) was digested with restriction enzyme *Bam*HI, which was ligated with the partially degraded chromosomal DNA fragments. DNA ligation was performed by using DNA ligation kit (produced by Takara Shuzo) in accordance with a designated method. After that, *Escherichia coli* JM109 (produced by Takara Shuzo) was transformed with an obtained DNA mixture in accordance with an ordinary method. Transformants were plated on an L agar medium containing 100 µg/ml of ampicillin, and they were grown to prepare a gene library.

A reaction solution containing 4 mM p-nitrophenylphosphoric acid and 100 mM MES/NaOH buffer (pH 6.5) was poured onto a surface of the agar medium on which the transformants had grown, and the temperature was kept at 30 °C for 15 minutes. Strains which had expressed the phosphatase activity liberated p-nitrophenol and exhibited a yellow color. Accordingly, transformants were selected by using this phenomenon as an index. As a result of screening for a gene expression library comprising about 20,000 strains of transformants, 30 strains of transformants which had expressed the phosphatase activity were obtained.

The transformants (30 strains), which had expressed the phosphatase activity, were subjected to single colony isolation. Single colonies were inoculated to an L-medium (2.5 ml) containing 100 µg/ml of ampicillin, and they were cultivated at 37 °C for 16 hours. Sodium acetate buffer (100 mM, pH 5.0, 50 µl) containing inosine (2 g/dl) and sodium pyrophosphate (10 g/dl) was added to microbial cells harvested from culture, and the reaction mixture was incubated at 30 °C for 16 hours. Production of 5'-inosinic acid was detected by HPLC analysis to select microbial strains having the transphosphorylation activity. As a result, we succeeded in obtaining 5 strains of transformants which exhibited the transphosphorylation activity and which were assumed to harbor a DNA fragment containing the objective acid phosphatase gene.

30 Example 8: Determination of Nucleotide Sequence of Acid Phosphatase Gene Derived from *Morganella morganii* NCIMB 10466

The inserted DNA fragment was analyzed by preparing a plasmid in accordance with an alkaline lysis method (*Molecular Cloning 2nd edition* (J. Sambrook, E. F. Fritsch and T. Maniatis, Cold Spring Harbour Laboratory Press, pl. 25 (1989)) from one strain of the transformants which were assumed to harbor the DNA fragment containing the acid phosphatase gene derived from *Morganella morganii* NCIMB 10466 obtained in Example 7. This plasmid was designated as pMPI501. Fig. 3 shows a determined restriction enzyme map of the inserted DNA fragment.

The region of the acid phosphatase gene was further specified by subcloning. As a result, it was suggested that this acid phosphatase gene was contained in a fragment having a size of 1.2 Kbp excised by restriction enzymes *Hind*III and *Eco*RI. Thus in order to determine the nucleotide sequence, plasmid DNA was constructed in which the fragment of 1.2 kbp was ligated with pUC118 having been digested with *Hind*III and *Eco*RI. *Escherichia coli* JM109 (produced by Takara Shuzo) was transformed with this plasmid DNA designated as pMPI505 in accordance with an ordinary method, which was plated on an L agar medium containing 100 µg/ml of ampicillin to obtain a transformant.

The plasmid was extracted in accordance with the alkaline lysis method from the transformant of *Escherichia coli* JM109 (produced by Takara Shuzo) harboring pMPI505 to determine the nucleotide sequence. The nucleotide sequence was determined in accordance with a method of Sanger (*J. Mol. Biol.*, 143, 161 (1980)) by using Taq DyeDeoxy Terminator Cycle Sequencing Kit (produced by Applied Biochemical). A nucleotide sequence of a determined open reading frame is shown in SEQ ID NO: 2 in Sequence Listing. An amino acid sequence of the protein deduced from the nucleotide sequence is shown in SEQ ID NO: 3 in Sequence Listing. A partial sequence, which was completely coincident with the N-terminal amino acid sequence of the purified enzyme, was found in the amino acid sequence. The N-terminal of the purified enzyme starts from the 21th alanine residue of the sequence shown in SEQ ID NO: 3. Accordingly, it is assumed that the amino acid sequence shown in SEQ ID NO: 3 is that of a precursor protein, and that a peptide comprising a range from the 1st methionine residue to the 20th alanine residue is eliminated after translation. An amino acid sequence of a mature protein thus deduced is shown in SEQ ID NO: 4 in Sequence Listing. A molecular weight of the mature protein estimated from the amino acid sequence is calculated to be 24.9 kilodaltons, which is well coincident with the result of SDS-PAGE for the purified enzyme. According to the results described above, and because of the fact that the transformant harboring the plasmid containing this fragment exhibited the transphos-

phorylation activity, it was identified that this open reading frame was the region coding for the objective acid phosphatase.

The nucleotide sequence and the amino acid sequence were respectively compared with known sequences for homology. Data bases of EMBL and SWISS-PROT were used. As a result, it has been revealed that the nucleotide sequence shown in SEQ ID NO: 2 in Sequence Listing is coincident with a nucleotide sequence of a known acid phosphatase gene derived from *Morganella morganii* (Thaller, M. C. et al., *Microbiology*, 140, 1341 (1994)) except that 54th G is A, 72th G is A, 276th T is G, 378th T is C, 420th G is T, 525th C is G, 529th C is T, and 531th G is A in the latter, and that the amino acid sequence shown in SEQ ID NO: 4 in Sequence Listing is the same as that of the acid phosphatase gene derived from *Morganella morganii*. Namely, the gene, which codes for the protein comprising the amino acid sequence shown in SEQ ID NO: 4 in Sequence Listing, is the acid phosphatase gene of *Morganella morganii* NCIMB 10466.

A precursor protein comprises 249 amino acids, and a molecular weight of the protein deduced from its sequence is 27.0 kilodaltons.

The strain of *Escherichia coli* JM109 transformed by a plasmid pMPI505, has been designated as AJ13143, which has been internationally deposited on February 23, 1996 in National Institute of Bioscience and Human Technology of Agency of Industrial Science and Technology (postal code: 305, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) under the provision of the Budapest Treaty, and awarded a deposition number of FERM BP-5422.

Example 9: Amplification of Activity by Expressing Gene of Acid Phosphatase Derived from *Morganella morganii* NCIMB 10466

Escherichia coli JM109/pMPI505 constructed in Example 8 was inoculated to an L-medium (50 ml) containing 100 µg/ml of ampicillin and 1 mM of IPTG, and it was cultivated at 37 °C for 16 hours. Microbial cells were harvested from its culture by centrifugation, and they were washed once with physiological saline. The microbial cells were suspended in 100 mM potassium phosphate buffer (5 ml, pH 7.2), and they were disrupted by means of a ultrasonic treatment performed at 4 °C for 20 minutes. The treated solution was centrifuged to remove an insoluble fraction, and thus, a cell-free extract was prepared.

The transphosphorylation activity of the obtained cell-free extract was measured while using controls of cell-free extracts prepared from the wild type strain of *Morganella morganii* and *Escherichia coli* JM109 transformed with the plasmid pUC118 in the same manner as described above. A result is shown in Table 7. The transphosphorylation activity was not detected in *Escherichia coli* JM109/pUC118. The transphosphorylation activity was also low in the wild type strain of *Morganella morganii*. On the other hand, *Escherichia coli* JM109/pMPI505 exhibited a high transphosphorylation activity which was 150 times as high as that of the wild type strain of *Morganella morganii* in specific activity. According to the result, it has been demonstrated that the introduced DNA fragment allows *Escherichia coli* to express the acid phosphatase at a high level.

Table 7

Microbial strain	Transphosphorylation Activity (units/mg)
<i>Morganella morganii</i> NCIMB 10466	0.008
<i>Escherichia coli</i> JM109/pUC118	not detected
<i>Escherichia coli</i> JM109/pMPI505	1.250

Example 11: Isolation of Gene Coding for Acid Phosphatase from Chromosome of *Escherichia blattae*

(1) Determination of N-terminal amino acid sequence

The acid phosphatase purified from the cell-free extract of *Escherichia blattae* JCM 1650 was adsorbed to DITC membrane (produced by Milligen/Bioscience), and its N-terminal amino acid sequence was determined by using Pros-sequencer 6625 (produced by Milligen/Bioscience). An N-terminal amino acid sequence comprising 15 residues shown in SEQ ID NO: 8 in Sequence Listing was determined.

(2) Isolation of DNA fragment containing gene coding for acid phosphatase

Chromosomal DNA was extracted from cultivated cells of *Escherichia blattae* JCM 1650 in accordance with a method of Murray and Thomson (*Nucl. Acid Res.*, 4321, 8 (1980)). The chromosomal DNA was partially degraded with *Sau*3AI. After that, DNA fragments of 3 to 6 kbp were fractionated by means of sucrose density gradient centrifugation.

A plasmid vector pUC118 (produced by Takara Shuzo) was digested with BamHI, which was ligated with the partially degraded chromosomal DNA fragments. DNA ligation was performed by using DNA ligation kit (produced by Takara Shuzo) in accordance with a designated method. After that, Escherichia coli JM109 (produced by Takara Shuzo) was transformed with an obtained DNA mixture in accordance with an ordinary method. Transformants were plated on an L agar medium containing 100 µg/ml of ampicillin, and they were grown to prepare a gene library.

A reaction solution containing 4 mM p-nitrophenylphosphoric acid and 100 mM MES/NaOH buffer (pH 6.5) was poured onto a surface of the agar medium on which the transformants had grown, and the temperature was kept at 30 °C for 15 minutes. Strains which had expressed the phosphatase activity liberated p-nitrophenol and exhibited a yellow color. Accordingly, transformants were selected by using this phenomenon as an index. As a result of screening for a chromosomal gene expression library comprising about 8,000 strains of transformants, 14 strains of transformants which had expressed the phosphatase activity were obtained.

The transformants (14 strains), which had expressed the phosphatase activity, were subjected to single colony isolation. Single colonies were inoculated to an L-medium (2.5 ml) containing 100 µg/ml of ampicillin, and they were cultivated at 37 °C for 16 hours. Sodium acetate buffer (100 mM, pH 5.0, 50 µl) containing inosine (2 g/dl) and sodium pyrophosphate (10 g/dl) was added to microbial cells harvested from culture liquids to perform the reaction at 30 °C for 16 hours. Production of 5'-inosinic acid was detected by HPLC analysis to select strains having the transphosphorylation activity. As a result, we succeeded in obtaining 3 strains of transformants which exhibited the transphosphorylation activity and which were assumed to harbor a DNA fragment containing the objective acid phosphatase gene.

Example 12: Determination of Nucleotide Sequence of Acid Phosphatase Gene Derived from Escherichia blattae JCM 1650

The inserted DNA fragment was analyzed by extracting a plasmid in accordance with the alkaline lysis method from one strain of the transformants which were assumed to harbor the DNA fragment containing the acid phosphatase gene derived from Escherichia blattae JCM 1650 obtained in Example 11. This plasmid was designated as pEPI301. Fig. 5 shows a determined restriction enzyme map of the inserted DNA fragment.

The region of the acid phosphatase gene was further specified by subcloning. As a result, it was suggested that this acid phosphatase gene was included in a fragment having a size of 2.4 Kbp excised by restriction enzymes Clal and BamHI. Thus in order to determine the nucleotide sequence, plasmid DNA was constructed in which the fragment was ligated with pBluescript KS(+) (produced by Stratagene) having been digested with Clal and BamHI. Escherichia coli JM109 (produced by Takara Shuzo) was transformed with the plasmid DNA designated as pEPI305 in accordance with an ordinary method, which was plated on an L agar medium containing 100 µg/ml of ampicillin to obtain a transformant.

The plasmid was extracted in accordance with the alkaline lysis method from the transformant of Escherichia coli JM109 (produced by Takara Shuzo) harboring pEPI305 to determine the nucleotide sequence. A nucleotide sequence of a determined open reading frame is shown in SEQ ID NO: 6 in Sequence Listing. An amino acid sequence of the protein deduced from the nucleotide sequence is shown in SEQ ID NO: 7 in Sequence Listing. A partial sequence, which was completely coincident with the N-terminal amino acid sequence of the purified enzyme, was found in the amino acid sequence. The N-terminal of the purified enzyme starts from the 19th leucine residue of the sequence shown in SEQ ID NO: 7. Accordingly, it is assumed that the amino acid sequence shown in SEQ ID NO: 7 is that of a precursor protein and that a peptide comprising a range from the 1st methionine residue to the 18th alanine residue is eliminated after translation. An amino acid sequence of a mature protein thus deduced is shown in SEQ ID NO: 8 in Sequence Listing. Accordingly, an estimated molecular weight of the mature protein is calculated to be 25.1 kilodaltons, which is well coincident with the result of SDS-PAGE for the purified enzyme. According to the results described above, and because of the fact that the transformant harboring the plasmid containing this fragment exhibited the transphosphorylation activity, it was identified that this open reading frame was the region coding for the objective acid phosphatase.

Namely, the gene, which codes for the protein comprising the amino acid sequence shown in SEQ ID NO: 8 in Sequence Listing, is the acid phosphatase gene of Escherichia blattae JCM.1650.

The nucleotide sequence and the amino acid sequence were respectively compared with known sequences for homology. Data bases of EMBL and SWISS-PROT were used. As a result, it has been revealed that the protein shown in SEQ ID NO: 8 and DNA coding for it are novel. A precursor protein encoded by this gene comprises 249 amino acids, and a molecular weight of the protein deduced from its sequence is 27.0 kilodaltons.

The amino acid sequence was compared with known sequences respectively for homology. As a result, this protein exhibited a high degree of homology with the acid phosphatase of Providencia stuartii (77.1 %) with the acid phosphatase of Morganella morganii in Example 8 (77.1 %), and with acid phosphatase of Salmonella typhimurium (44.3 %).

The strain of Escherichia coli JM109 transformed by a plasmid pEPI305, has been designated as AJ13144, which has been internationally deposited on February 23, 1996 in National Institute of Bioscience and Human Technology of

Agency of Industrial Science and Technology (postal code: 305, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) under the provision of the Budapest Treaty, and awarded a deposition number of FERM BP-5423.

Example 13: Amplification of Activity by Expressing Gene of Acid Phosphatase Derived from *Escherichia blattae* JCM 1650

Escherichia coli JM109/pEPI305 constructed in Example 12 was inoculated to an L medium (50 ml) containing 100 µg/ml of ampicillin and 1 mM of IPTG, and it was cultivated at 37 °C for 16 hours. Microbial cells were harvested from its culture by centrifugation, and they were washed once with physiological saline. The microbial cells were suspended in 100 mM potassium phosphate buffer (5 ml, pH 7.2), and were disrupted by means of a ultrasonic treatment performed at 4 °C for 20 minutes. The treated solution was centrifuged to remove an insoluble fraction, and thus a cell-free extract was prepared.

The transphosphorylation activity of the obtained cell-free extract was measured while using controls of cell-free extracts prepared from the wild type strain of *Escherichia blattae* and *Escherichia coli* JM109 transformed with the plasmid pBluescript KS(+) in the same manner as described above. A result is shown in Table 8. The transphosphorylation activity was not detected in *Escherichia coli* JM109/pBluescript KS(+). The transphosphorylation activity was also low in the wild type strain of *Escherichia blattae*. On the other hand, *Escherichia coli* JM109/pEPI305 exhibited a high transphosphorylation activity which was 120 times as high as that of the wild type strain of *Escherichia blattae* in specific activity. According to the result, it has been demonstrated that the introduced DNA fragment allows *Escherichia coli* to express the acid phosphatase at a high level.

Table 8

Microbial strain	Transphosphorylation Activity (units/mg)
<i>Escherichia blattae</i> JCM 1650	0.002
<i>Escherichia coli</i> JM109/pBluescript KS(+)	not detected
<i>Escherichia coli</i> JM109/pEPI305	0.264

Example 14: Production of 5'-Inosinic Acid from Inosine by Using Strain Harboring Acid Phosphatase Gene Derived from *Escherichia blattae* JCM 1650

Sodium pyrophosphate (12 g/dl) and inosine (6 g/dl) were dissolved in 100 mM sodium acetate buffer (pH 4.0), to which the microbial cells of *Escherichia coli* JM109/pEPI305 described above were added to give a cell concentration of 200 mg/dl as converted into a dry weight of the microbial cells. The reaction mixture was incubated at 35 °C for 10 hours while maintaining pH at 4.0, and the amount of produced 5'-inosinic acid was measured along with passage of time. Produced inosinic acid contained only 5'-inosinic acid. By-production of 2'-inosinic acid and 3'-inosinic acid was not observed at all. A result is shown in Fig. 6. 5'-Inosinic acid was produced and accumulated extremely efficiently in a short period of time in the reaction to produce 5'-inosinic acid from pyrophosphate and inosine by using this microorganism.

Example 15: Preparation of A Gene Encoding An Acid Phosphatase with lowered Phosphomonoesterase activity

As described in Examples 13 and 14, the strain harboring the acid phosphatase gene derived from *Escherichia blattae* expresses a considerable amount of the acid phosphatase, and 5'-inosinic acid is produced and accumulated extremely efficiently in a short period of time in the reaction to produce 5'-inosinic acid from pyrophosphate and inosine by using this microorganism. However, it has been revealed that the accumulated amount of 5'-inosinic acid does not exceed a certain degree because produced 5'-inosinic acid undergoes degradation by the phosphomonoesterase activity possessed by the acid phosphatase itself. Thus the enzyme was intended to be improved by introducing mutation into the acid phosphatase gene derived from *Escherichia blattae* cloned in Example 11, in accordance with the site-directed mutagenesis method by using PCR.

Oligonucleotides MUT300, MUT310, and MUT320 shown in SEQ ID NOs: 9, 10, and 11 in Sequence Listing were synthesized respectively in accordance with the phosphoramidite method by using a DNA synthesizer (Model 394 produced by Applied Biosystems).

The plasmid pEPI305 (1 ng) as a template prepared in Example 12, M13 primer RV (produced by Takara Shuzo) and MUT310 oligonucleotide (each 2.5 µmol) as primers, and Taq DNA polymerase (2.5 units, produced by Takara Shuzo) were added to 100 mM Tris-HCl buffer (pH 8.3, 100 µl) containing dATP, dCTP, dGTP, dTTP (each 200 µM), potassium chloride (50 mM), and magnesium chloride (1.5 mM) to perform a PCR reaction in which a cycle comprising

periods of 30 seconds at 94 °C, 2 minutes at 55 °C, and 3 minutes at 72 °C was repeated 25 times. The PCR reaction was performed by using Thermal Cycler PJ2000 type (produced by Takara Shuzo). Also, a PCR reaction was performed in the same manner as described above by using plasmid pEPI305 (1 ng) as a template, and M13 primer M3 (produced by Takara Shuzo) and MUT300 oligonucleotide (each 2.5 µmol) as primers. Each of the reaction solutions was purified by gel filtration to remove the primers by using Micro spin column S-400 (produced by Pharmacia).

Each of the PCR reaction products (1 µl) was added to 100 mM Tris-HCl buffer (pH 8.3, 95 µl) containing dATP, dCTP, dGTP, dTTP (each 200 µM), potassium chloride (50 mM), and magnesium chloride (1.5 mM), and it was heated at 94 °C for 10 minutes, followed by cooling to 37 °C over 60 minutes. After that, the temperature was kept at 37 °C for 15 minutes to form a heteroduplex. Taq DNA polymerase (2.5 units) was added thereto to perform a reaction at 72 °C for 3 minutes so that the heteroduplex was completed. After that, M13 primer RV and M13 primer M3 (each 2.5 µmol) were added to this reaction solution to perform a PCR reaction in which a cycle comprising periods of 30 seconds at 94 °C, 2 minutes at 55 °C, and 3 minutes at 72 °C was repeated 10 times.

A product of the second PCR reaction was digested with ClaI and BamHI followed by phenol/chloroform extraction and ethanol precipitation. This DNA fragment was ligated with pBluescript KS(+) having been digested with ClaI and BamHI. *Escherichia coli* JM109 (produced by Takara Shuzo) was transformed with obtained plasmid DNA in accordance with an ordinary method, which was plated on an L agar medium containing 100 µg/ml of ampicillin to obtain a transformant.

The plasmid was extracted from the transformant in accordance with the alkaline lysis method to determine its nucleotide sequence, confirming that the objective nucleotide was substituted. Thus a mutant gene coding for a mutant phosphatase was prepared in which the 74th glycine residue (GGG) of the mature protein was substituted with an aspartic acid residue (G*A*T). The plasmid containing this mutant gene was designated as pEPI310.

A mutant gene coding for a mutant phosphatase was prepared in which the 153th isoleucine residue (ATC) of the mature protein was substituted with a threonine residue (A*CC), in accordance with the same procedure as described above by using pEPI305 as a template, and MUT300 and MUT320 oligonucleotides as primers. The plasmid containing this mutant gene was designated as pEPI320. Further, a mutant gene coding for a mutant phosphatase was prepared in which the 74th glycine residue (GGG) of the mature protein was substituted with an aspartic acid residue (G*A*T), and the 153th isoleucine residue (ATC) of the mature protein was substituted with a threonine residue (A*CC), in accordance with the same procedure as described above by using pEPI310 as a template, and MUT300 and MUT320 oligonucleotides as primers. The plasmid containing this mutant gene was designated as pEPI330.

Escherichia coli JM109/pEPI310, *Escherichia coli* JM109/pEPI320, and *Escherichia coli* JM109/pEPI330 into which the plasmids containing the respective mutant acid phosphatase genes had been introduced, and *Escherichia coli* JM109/pEPI305 into which the plasmid containing the wild type acid phosphatase gene had been introduced were inoculated to an L medium (50 ml) containing 100 µg/ml of ampicillin and 1 mM of IPTG, and they were cultivated at 37 °C for 16 hours. Microbial cells were harvested from their culture, and they were washed once with physiological saline. The microbial cells were suspended in 100 mM potassium phosphate buffer (5 ml, pH 7.0), and they were disrupted by means of a ultrasonic treatment performed at 4 °C for 20 minutes. The treated solutions were centrifuged to remove insoluble fractions, and thus cell-free extracts were prepared. Phosphomonoesterase activities and transphosphorylation activities of the obtained cell-free extracts were measured at pH 4.0, and they were compared with an activity of the wild strain.

Table 9 shows the result of measurement of phosphomonoesterase activities and transphosphorylation activities of wild type acid phosphatase and acid phosphatases with lowered phosphomonoesterase activity. It shows that both of phosphomonoesterase activities and transphosphorylation activities of acid phosphatases with lowered phosphomonoesterase activity are lowered as compared with wild type acid phosphatase, and that degrees of decrease of phosphomonoesterase activities are larger than that of transphosphorylation activities, with the result that a ratio of phosphomonoesterase activity to transphosphorylation activity of the mutant acid phosphatase is lowered in comparison with the wild type acid phosphatase.

Table 9

Plasmid	Phosphomonoesterase activity (units/mg)	Transphosphorylation activity (units/mg)	Ratio ¹⁾ (Relative value)
pEPI305	2.38	0.132	18.03 (100)

¹⁾: Ratio of phosphomonoesterase activities to the activities to produce nucleoside-5'-phosphate ester

Table 9 (continued)

Plasmid	Phosphomonoesterase activity (units/mg)	Transphosphorylation activity (units/mg)	Ratio ¹⁾ (Relative value)
pEPI310	0.26	0.019	13.68(76)
pEPI320	0.88	0.123	7.15(39)
pEPI330	0.42	0.070	6.00(33)

1) Ratio of phosphomonoesterase activities to the activities to produce nucleoside-5'-phosphate ester

Example 16: Production of 5'-Inosinic Acid from Inosine by Using The Strains Harboring A Gene Encoding The Acid Phosphatase with Lowered Phosphomonoesterase Activity

Escherichia coli JM109/pEPI310, *Escherichia coli* JM109/pEPI320, and *Escherichia coli* JM109/pEPI330 into which the plasmids containing the genes encoding the acid phosphatases with lowered phosphomonoesterase activity had been introduced, and *Escherichia coli* JM109/pEPI305 into which the plasmid containing the wild type acid phosphatase gene had been introduced were inoculated to an L medium (50 ml) containing 100 µg/ml of ampicillin and 1 mM of IPTG, and they were cultivated at 37 °C for 16 hours.

Sodium pyrophosphate (12 g/dl) and inosine (6 g/dl) were dissolved in sodium acetate buffer (pH 4.0), to which microbial cells of each of the strains of *Escherichia coli* obtained by the cultivation described above were added to give a cell concentration of 200 mg/dl as converted into a dry weight of the microbial cells. The reaction mixture was incubated at 35 °C for 32 hours while maintaining pH at 4.0, and the amount of produced 5'-inosinic acid was measured along with passage of time. A result is shown in Fig. 8.

In Fig. 7, the axis of ordinate indicates the concentration of 5'-inosinic acid (mg/dl), and the axis of abscissa indicates the reaction time (h). Progress of the reaction is indicated by solid circles for *Escherichia coli* JM109/pEPI305, solid triangles for *Escherichia coli* JM109/pEPI310, blanked circles for *Escherichia coli* JM109/pEPI320, and blanked squares for *Escherichia coli* JM109/pEPI330, as measured by using the cells of the respective strains.

The velocity of degradation of produced 5'-inosinic acid was decreased in the reaction to produce 5'-inosinic acid from inosine by using the strains harboring the acid phosphatase with lowered phosphomonoesterase activity. As a result, the yield and the accumulated amount of 5'-inosinic acid were increased. The highest accumulation of 5'-inosinic acid was exhibited by *Escherichia coli* JM109/pEPI330 as the strain harboring the gene encoding the acid phosphatase with lowered phosphomonoesterase activity in which the 74th glycine residue and the 153th isoleucine residue were substituted with the aspartic acid residue and the threonine residue respectively.

Example 17: Production of Various Nucleoside-5'-Phosphate Esters by Using The Strains Harboring A Gene Encoding The Acid Phosphatase with Lowered Phosphomonoesterase Activity

Escherichia coli JM109/pEPI330 into which the plasmid containing the gene encoding the acid phosphatase with lowered phosphomonoesterase activity had been introduced was inoculated to an L medium (50 ml) containing 100 µg/ml of ampicillin and 1 mM of IPTG, and it was cultivated at 37 °C for 16 hours.

Sodium pyrophosphate (12 g/dl), and inosine, guanosine, uridine, or cytidine (6 g/dl) as a phosphate group acceptor were dissolved in 100 mM sodium acetate buffer (pH 4.0), to which the microbial cells described above were added to give a cell concentration of 200 mg/dl as converted into a dry weight of the cells. The reaction mixture was incubated at 35 °C for 32 hours while maintaining pH at 4.0. Amounts of produced nucleoside-5'-phosphate esters are shown in Table 10. Produced nucleotide contained only nucleoside-5'-phosphate ester. By-production of nucleoside-2'-phosphate ester and nucleoside-3'-phosphate ester was not observed at all.

Table 10

Nucleoside	Product	Produced amount (g/dl)
Inosine	5'-inosinic acid	7.45
Guanosine	5'-guanylic acid	4.77
Uridine	5'-uridylic acid	8.93
Cytidine	5'-cytidylic acid	6.60

Example 18: Production of 5'-Inosinic Acid from Various Phosphate Compounds as Phosphate Group Donors by Using The Strain Harboring A Gene Encoding The Acid Phosphatase with Lowered Phosphomonoesterase Activity

Escherichia coli JM109/pEPI330 into which the plasmid containing the mutant acid phosphatase gene had been introduced was inoculated to an L medium (50 ml) containing 100 µg/ml of ampicillin and 1 mM of IPTG, and it was cultivated at 37 °C for 16 hours.

Inosine (6 g/dl) and sodium tripolyphosphate, sodium polyphosphate (trade name: Polygon P, produced by Chiyoda Chemical), disodium phenylphosphate, or disodium carbamyl phosphate (12 g/dl) as a phosphate group donor were dissolved in 100 mM sodium acetate buffer (pH 4.0), to which the microbial cells described above were added to give a cell concentration of 200 mg/dl as converted into a dry weight of the cells. The reaction mixture was incubated at 35 °C for 32 hours while maintaining pH at 4.0. The amount of produced 5'-inosinic acid is shown in Table 11. 5'-Inosinic acid was efficiently produced and accumulated by using any of the phosphate group donors. However, the accumulated amount of 5'-inosinic acid was the highest when polyphosphoric acid was used as the phosphate group donor.

Table 11

Phosphate group donor	Produced 5'-inosinic acid (g/dl)
Sodium tripolyphosphate	5.96
Sodium polyphosphate	8.84
Disodium phenylphosphate	7.60
Disodium carbamyl phosphate	7.73

Example 19

Studies on production of a new mutant acid phosphatase gene derived from *E. blattae* JCM1650 and enzymological properties of the mutant acid phosphatase gene:

In Examples 19 to 22, the transphosphorylation activity to a nucleoside was measured under the following conditions. The reaction was conducted at 30°C and a pH of 4.0 for 10 minutes using 1 ml of a reaction solution containing 40 µmol/ml of inosine, 100 µmol/ml of sodium pyrophosphate, 100 µmol/ml of a sodium acetate buffer (pH 4.0) and an enzyme. This reaction was terminated with the addition of 200 µl of 2-N hydrochloric acid. Then, the precipitate was removed through centrifugation, and the amount of 5'-inosinic acid formed through the transphosphorylation was determined under the above-mentioned conditions. The amount of the enzyme with which to produce 1 µmol of inosinic acid under these standard reaction conditions was defined as 1 unit.

Further, the transphosphorylation activity was measured by changing the inosine concentration from 10 to 100 µmol/ml under the reaction conditions of the above-mentioned composition, and the rate constant of inosine in the transphosphorylation activity was determined using the Hanes-Woolf plot [Biochem. J., 26, 1406 (1932)].

As described later, the detailed analysis was conducted with respect to the mutant enzyme by which to improve the productivity of the nucleoside-5'-phosphate ester described in Example 15. Consequently, it was found that the affinity for nucleoside of the mutant enzyme was improved by 2 times as compared with that of the wild-type enzyme. Therefore, the present inventors considered that the productivity of the nucleoside-5'-phosphate ester would be improved by increasing the affinity for nucleoside of the above-mentioned enzyme, and they further modified the enzyme by the genetic engineering method.

Plasmid pEPI305 containing the gene encoding the wild-type acid phosphatase derived from *E. blattae* described in Example 15 was used, and the site specific mutation was introduced into this plasmid DNA by the genetic engineering method to produce a gene encoding the mutant acid phosphatase. pEPI305 is a plasmid DNA formed by binding a DNA fragment of 2.4 Kbp cleaved with restriction endonucleases ClaI and BamHI and containing a gene encoding a wild-type acid phosphatase derived from *E. blattae* JCM1650 to pBluescript KS(+) (supplied by Stratagene) cleaved with ClaI and BamHI. The base sequence of the gene encoding the acid phosphatase is represented by SEQ ID NO: 6 in Sequence Listing. Further, an amino acid sequence of a precursor protein anticipated from this base sequence is represented by SEQ ID NO: 7 in Sequence Listing. From the analytical results of the purified enzyme (described in Example 4), the amino acid sequence of the maturation protein is presumed to be represented by SEQ ID NO: 8 in Sequence Listing.

Oligonucleotides MUT300 (SEQ ID NO: 9 in Sequence Listing), MUT310 (SEQ ID NO: 10 in Sequence Listing), MUT320 (SEQ ID NO: 11 in Sequence Listing), MUT330 (SEQ ID NO: 12 in Sequence Listing), MUT340 (SEQ ID NO: 13 in Sequence Listing), MUT350 (SEQ ID NO: 14 in Sequence Listing), MUT360 (SEQ ID NO: 15 in Sequence Listing), MUT370 (SEQ ID NO: 16 in Sequence Listing), MUT380 (SEQ ID NO: 17 in Sequence Listing) and MUT390 (SEQ ID NO: 18 in Sequence Listing) having the sequences shown in Sequence Listing were synthesized by the phosphoramidite method using a DNA synthesizer (Model 394 supplied by Applied Biosystem).

One nanogram of pEPI305 as a template, 2.5 µmols of M13 Primer RV (supplied by Takara Shuzo Co., Ltd.), 2.5

μmols of oligonucleotide MUT310 and 2.5 units of tac DNA polymerase (supplied by Takara Shuzo Co., Ltd.) were added to 100 μl of a Tris-hydrochloride buffer (pH 8.3) containing 200 μM of dATP, 200 μM of dCTP, 200 μM of dGTP, 200 μM of dTTP, 50 mM of potassium chloride and 1.5 mM of magnesium chloride. PCR was conducted in which a three-part step, namely, at 94°C for 30 seconds, at 55°C for 2 minutes and at 72°C for 3 minutes was repeated 25 times. In this reaction, a thermal cycler PJ2000 model (supplied by Takara Shuzo Co., Ltd.) was used. Separately, PCR was likewise conducted using 1 ng of plasmid DNA pEPI305 as a template, 2.5 μmols of M13 Primer M3 (supplied by Takara Shuzo Co., Ltd.) as a primer and 2.5 μmols of oligonucleotide MUT300. Each of the reaction solutions was purified through gel filtration using a microspin column S-400 (supplied by Pharmacia) to remove the primer.

One microliter of each of the PCR solutions was added to 95 μl of a 100-mM Tris-hydrochloride buffer (pH 8.3) containing 200 μM of dATP, 200 μM of dCTP, 200 μM of dGTP, 200 μM of dTTP, 50 mM of potassium chloride and 1.5 mM of magnesium chloride. The mixture was heated at 94°C for 10 minutes, then cooled to 37°C over the course of 60 minutes, and warmed at 37°C for 15 minutes to form a heteroduplex. To this were added 2.5 units of tac DNA polymerase, and the reaction was conducted at 72°C for 3 minutes to complete the heteroduplex. Subsequently, 2.5 μmols of M13 Primer RV and 2.5 μmols of M13 Primer M3 were added to the reaction solution, and PCR was conducted in which a three-part step, namely, at 94°C for 30 seconds, at 55°C for 2 minutes and at 72°C for 3 minutes was repeated 10 times.

The second PCR product was cleaved with ClaI and BamHI, then extracted with a mixture of phenol and chloroform, and precipitated with ethanol. This DNA fragment was bound to pBluescript KS (+) cleaved with ClaI and BamHI. E. coli JM109 (supplied by Takara Shuzo Co., Ltd.) was transformed in a usual manner using the resulting plasmid DNA. This was plated on an L agar medium containing 100 μg/ml of ampicillin to obtain a transformant. A plasmid was prepared from the transformant by an alkali bacteriolysis method, the base sequence was determined, and it was identified that the desired base was substituted. The determination of the base sequence was conducted by the method of Sanger et al. [J. Mol. Biol., 143, 161 (1980)] using a Taq DyeDeoxy Terminator Cycle Sequencing Kit (supplied by Applied Biochemical). In this manner, the mutant gene encoding the mutant phosphatase in which the 74th glycine residue (GGG) of the maturation protein was substituted with the aspartic acid residue (G*A*T) was produced. This mutant gene-containing plasmid was designated pEPI310 (Example 15).

The above-mentioned procedure was repeated using the plasmid having the mutation introduced therein as a template to cumulatively introduce the site-specific mutation. A plasmid was produced from the transformant by the alkali bacteriolysis method, the base sequence was determined, and it was identified that the desired base was substituted. The resulting mutant genes encoding the mutant phosphatase and the mutation sites are shown in Table 12. The amino acid residue in the mutation site indicates an amino acid residue in the amino acid sequence of the mature protein represented by SEQ ID NO: 8 in Sequence Listing.

Table 12

plasmid name	starting material	primer	mutation position and substituted amino acid
pEPI305	-		wild type
pEPI310	pEPI305	MUT300	74Gly(GGG)→Asp(G*A*T)
		MUT310	
pEPI330	pEPI310	MUT300 MUT320	74Gly(GGG)→Asp(G*A*T) 153Ile(ATC)→Thr(A*CC)
pEPI340	pEPI330	MUT300 MUT330	63Leu(CTG)→Gln(C*AG) 65Ala(GCG)→Gln(*C*AG) 66Glu(GAA)→Ala(G*CA) 74Gly(GGG)→Asp(G*A*T) 153Ile(ATC)→Thr(A*CC)
pEPI350	pEPI340	MUT300 MUT340	63Leu(CTG)→Gln(C*AG) 65Ala(GCG)→Gln(*C*AG) 66Glu(GAA)→Ala(G*CA) 74Gly(GGG)→Asp(G*A*T) 85Ser(TCC)→Tvr(T*AC) 153Ile(ATC)→Thr(A*CC)
pEPI360	pEPI340	MUT300 MUT350	63Leu(CTG)→Gln(C*AG) 65Ala(GCG)→Gln(*C*AG)

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Table 12 (continued)

plasmid name	starting material	primer	mutation position and substituted amino acid
			66Glu(GAA)→Ala(G*CA) 74Gly(GGG)→Asp(G*A*T) 135Thr(ACC)→Lys(A*A*A) 136Glu(GAG)→Asp(GA*C) 153Ile(ATC)→(A*CC)
pEPI370	pEPI360	MUT300 MUT360	63Leu(CTG)→Gln(C*AG) 65Ala(GCG)→Gln(*C*AG) 66Glu(GAA)→Ala(G*CA) 69Asn(AAC)→Asp(*GAC) 71Ser(AGC)→Ala(*G*CC) 72Ser(AGT)→Ala(*G*CT) 74Gly(GGG)→Asp(G*A*T) 135Thr(ACC)→Lys(A*A*A) 136Glu(GAG)→Asp(GA*C) 153Ile(ATC)→(A*CC)
pEPI380	pEPI370	MUT300 MUT370	63Leu(CTG)→Gln(C*AG) 65Ala(GCG)→Gln(*C*AG) 66Glu(GAA)→Ala(G*CA) 69Asn(AAC)→Asp(*GAC) 71Ser(AGC)→Ala(*G*CC) 72Ser(AGT)→Ala(*G*CT) 74Gly(GGG)→Asp(G*A*T) 116Asp(GAT)→Glu(GA*A) 135Thr(ACC)→Lys(A*A*A) 136Glu(GAG)→Asp(GA*C) 153Ile(ATC)→(A*CC)
pEPI390	pEPI380	MUT300 MUT380	63Leu(CTG)→Gln(C*AG) 65Ala(GCG)→Gln(*C*AG) 66Glu(GAA)→Ala(G*CA) 69Asn(AAC)→Asp(*GAC) 71Ser(AGG)→Ala(*G*CC) 72Ser(AGT)→Ala(*G*CT) 74Gly(GGG)→Asp(G*A*T) 116Asp(GAT)→Glu(GA*A) 130Ser(TCT)→Glu(*G*A*A) 135Thr(ACC)→Lys(A*A*A) 136Gln(GAG)→Asp(GA*C) 153Ile(ATC)→Thr(A*CC)
pEPI400	pEPI380	MUT300 MUT390	63Leu(CTG)→Gln(C*AG) 65Ala(GCG)→Gln(*C*AG) 66Glu(GAA)→Ala(G*CA) 69Asn(AAC)→Asp(*GAC) 71Ser(AGC)→Ala(*G*CC) 72Ser(AGT)→Aln(G*A*T) 74Gly(GGG)→Asp(G*A*T) 92Ala(GCC)→Ser(*A*GC) 94Ala(GCg)→Glu(G*A*A) 116Asp(GAT)→Glu(GA*A)

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Table 12 (continued)

plasmid name	starting material	primer	mutation position and substituted amino acid
			135Thr(ACC)→Lys(A*A*) 136Glu(GAG)→(GA*C) 153Ile(ATC)→Thr(A*CC)

Each of *E. coli* JM109/pEPI330, *E. coli* JM109/pEPI340, *E. coli* JM109/pEPI350, *E. coli* JM109/pEPI360, *E. coli* JM109/pEPI370, *E. coli* JM109/pEPI380, *E. coli* JM109/pEPI390 and *E. coli* JM109/pEPI400 each having introduced therein a plasmid containing the mutant acid phosphatase gene and *E. coli* JM109/pEPI305 having introduced therein a plasmid containing a wild-type acid phosphatase gene was inoculated into 50 ml of an L medium containing 100 µg/ml of ampicillin and 1 mM of IPTG, and incubated at 37°C for 16 hours. The cells were collected from 2 liters of the culture solution of each of the strains through centrifugation, and washed once with a physiological saline solution. The cells were suspended in 50 ml of a 100-mM phosphate buffer (pH 7.0), and sonicated at 4°C for 20 minutes to disrupt the cells. The thus-treated solution was centrifuged to remove insoluble fractions and prepare a cell-free extract. Each of the acid phosphatases was purified from each of the cell-free extracts by the method described in Example 4. Each of the enzyme products was uniform in the SDS-polyacrylamide electrophoresis.

The rate constant of inosine in the transphosphorylation of the purified mutant acid phosphatases and wild-type acid phosphatase was measured, and the results are shown in Table 13. It was found that the mutant enzyme expressed in *E. coli* JM109/pEPI330 having the improved productivity of the nucleoside-5'-phosphate ester as described in Example 15 has decreased Vmax but greatly decreased the Km value to inosine which means the increased affinity for inosine by twice or more as compared with the wild-type enzyme expressed in *E. coli* JM109/pEPI305. This suggested that the productivity of the nucleoside-5'-phosphate ester of this mutant enzyme was greatly improved not only because of the decrease in the nucleotidase activity but also because of the improvement in the affinity for nucleoside which was an important factor. Accordingly, it was expected that the increase in the affinity for nucleoside leads to the improvement in the productivity.

The new mutant enzymes expressed in *E. coli* JM109 having been introduced therein with the new mutant enzyme gene produced in this Example exhibited the affinity for inosine which was more improved than that of *E. coli* JM109/pEPI330 described in Example 15. Thus, it was expected that the productivity of the nucleoside-5'-phosphate ester was improved. Further, the mutant enzyme expressed in *E. coli* JM109/pEPI380 not only improved the affinity for inosine but also increased the Vmax value as compared with the wild-type enzyme. Still further, it was expected that the productivity of the nucleoside-5'-phosphate ester was improved.

Table 13

Strain of an enzyme	Km(mM)	Vmax(unit/mg)
<i>E. coli</i> JM109/pEPI305	202	1.83
<i>E. coli</i> JM109/pEPI330	109	1.39
<i>E. coli</i> JM109/pEPI340	85	1.03
<i>E. coli</i> JM109/pEPI350	85	0.93
<i>E. coli</i> JM109/pEPI360	55	1.33
<i>E. coli</i> JM109/pEPI370	42	1.15
<i>E. coli</i> JM109/pEPI380	42	2.60
<i>E. coli</i> JM109/pEPI390	42	2.58
<i>E. coli</i> JM109/pEPI400	43	2.11

Example 20

Production of 5'-inosinic acid using a new mutant acid phosphatase gene-containing strain:

Each of *E. coli* JM109/pEPI330, *E. coli* JM109/pEPI340, *E. coli* JM109/pEPI360, *E. coli* JM109/pEPI370 and *E. coli* JM109/pEPI380 each having introduced therein the plasmid containing the mutant acid phosphatase gene was inoculated into 50 ml of an L medium containing 100 µg/ml of ampicillin and 1 mM of IPTG, and incubated at 37°C for 16 hours.

Pyrophosphoric acid (15 g/dl) and 8 g/dl of inosine were dissolved in an acetate buffer (pH 4.0). To the solution was added *E. coli* JM109 strain having introduced therein the above-mentioned mutant and wild-type acid phosphatase genes such that the concentration reached 200 mg/dl in terms of the dry cell weight. The reaction was conducted at

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35°C for 32 hours while maintaining the pH at 4.0, and the amount of 5'-inosinic acid formed over the course of time was measured. Inosinic acid formed was only 5'-inosinic acid, and the formation of 2'-inosinic acid and 3'-inosinic acid as by-products was not observed at all. The results are shown in Fig. 8.

E. coli JM109/pEPI330 described in Example 15 showed the accumulation of 5'-inosinic acid in a large amount. Although the substrate still remained, the formation of 5'-inosinic acid stopped when the amount of 5'-inosinic acid accumulated reached 7.5 g/dl, and the amount of 5'-inosinic acid was no longer increased. By contrast, the new mutant acid phosphatase gene-containing strains provided the large amount of 5'-inosinic acid accumulated. Especially, in the reaction using E. coli JM109/pEPI370 and E. coli JM109/pEPI380, the larger amount of 5'-inosinic acid accumulated was provided. In addition, the reaction rate was high, showing that the productivity of 5'-inosinic acid was further improved greatly. In particular, in E. coli JM109/pEPI380, the reaction rate was high, and quite a high reactivity was shown.

Example 21

Production of various nucleoside-5'-phosphate esters using a new mutant acid phosphatase gene-containing strain:

E. coli JM109/pEPI380 having introduced therein the plasmid containing the new mutant acid phosphatase gene was inoculated into 50 ml of an L medium containing 100 µg/ml of ampicillin and 1 mM of IPTG, and incubated at 37°C for 16 hours.

Pyrophosphoric acid (15 g/dl) and 8 g/dl of inosine, guanine, uridine or cytidine as a phosphate acceptor were dissolved in a 100-mM acetate buffer (pH 4.5). To this was added the above-mentioned strain such that the concentration reached 100 mg/dl in terms of the dry cell weight. The reaction was conducted at 35°C for 12 hours while maintaining the pH at 4.0. The amount of the nucleoside-5'-phosphate ester formed is shown in Table 4. The phosphorylation proceeded well with any of the nucleosides to form and accumulate the corresponding nucleoside-5'-phosphate esters. The nucleotide formed was only the nucleoside-5'-phosphate ester, and the formation of a nucleoside-2'-phosphate ester and a nucleoside-3'-phosphate ester as by-products was not observed at all.

Table 14

Nucleoside	Product	Amount of the Product (g/dl)
inosine	5'-inosinic acid	12.05
guanosine	5'-guanylic acid	5.78
uridine	5'-uridylic acid	13.28
cytidine	5'-cytidylic acid	10.65

Example 22

Production of 5'-inosinic acid using a new acid phosphatase gene-containing strain and various phosphoric acid compounds as a phosphate donor:

E. coli JM109/pEPI380 having introduced therein the plasmid containing the new mutant acid phosphatase gene was inoculated into 50 ml of an L medium containing 100 µg/ml of ampicillin and 1 mM of IPTG, and incubated at 37°C for 16 hours.

Inosine (6 g/dl) and 15 g/dl of a triphosphate, a polyphosphate ("Polygon P", a trade name for a product of Chiyoda Kagaku K.K.), disodium phenylacetate or disodium carbamylphosphate were dissolved in a 100-mM acetate buffer (pH 4.0). To this was added the above-mentioned strain such that the concentration reached 100 mg/dl in terms of the dry cell weight. The reaction was conducted at 35°C for 12 hours while maintaining the pH at 4.0. The amount of 5'-inosinic acid formed was shown in Table 15. 5'-Inosinic acid was formed and accumulated at good efficiency with any of the phosphate donors. Especially when a polyphosphate was used as a phosphate donor, 5'-inosinic acid was accumulated in the largest amount.

Table 15

Phosphate donor	Amount of 5'-inosinic acid formed (g/dl)
sodium triphosphate	10.84
sodium polyphosphate	13.35
disodium phenylphosphate	12.84
disodium carbamylphosphate	12.42

Table 15 (continued)

Phosphate donor	Amount of 5'-inosinic acid formed (g/dl)
potassium lithium acetylphosphate	10.65

Example 23: Isolation of Acid Phosphatase Gene Derived from Chromosome of *Providencia stuartii* and Determination of Nucleotide Sequence of the Gene

Oligonucleotides, PRP1 and PRP2, having nucleotide sequences illustrated in SEQ ID NO: 19 and 20 in Sequence Listing, respectively, were synthesized. These oligonucleotides are designed to amplify a gene coding for acid phosphatase of *Providencia stuartii* on the basis of known nucleotide sequence of the gene coding for acid phosphatase of *Providencia stuartii* (Database of EMBL Accession number X64820).

Chromosomal DNA was extracted from cultivated microbial cells of *Providencia stuartii* ATCC 29851 in accordance with a method of Murray and Thomson (Nucl. Acid Res., 4321, 8 (1980)). The chromosomal DNA (0.1 ng) as a template, oligonucleotides PRP1 and PRP2 (each 2.5 µmol) as primers, and Taq DNA polymerase (2.5 units, produced by Takara Shuzo) were added to 100 mM Tris-HCl buffer (pH 8.3, 100 µl) containing dATP, dCTP, dGTP, dTTP (each 200 µM), potassium chloride (50 mM), and magnesium chloride (1.5 mM) to perform a PCR reaction in which a cycle comprising periods of 30 seconds at 94 °C, 2 minutes at 55 °C, and 3 minutes at 72 °C was repeated 30 times. The reaction solution was subjected to agarose gel electrophoresis, followed by recovering the amplified DNA fragment of about 1 kbp by means of glass powders (made by Takara Shuzo). The gene fragment was digested with *Bam*HI, which was ligated with pUC118 digested with *Bam*HI. The plasmid obtained as described above was designated as pPRP100.

Phosphomonoesterase activity and transphosphorylation activity of *Escherichia coli* JM109/pPRP100, a transformant to which pPRP100 was introduced, were measured. As a result, the strain showed an activity to transphosphorylate to nucleoside as well as phosphomonoesterase activity.

The plasmid was extracted in accordance with the alkaline lysis method from the transformant of *Escherichia coli* JM109/pPRP100 to determine the nucleotide sequence. A nucleotide sequence of a determined open reading frame and an amino acid sequence of the protein deduced from the nucleotide sequence are shown in SEQ ID NO: 21 and 22 in Sequence Listing. The nucleotide sequence of the open reading frame is completely coincident with the nucleotide sequence of the known acid phosphatase gene of *Providencia stuartii*.

Example 24: Isolation of Acid Phosphatase Gene Derived from Chromosomes of *Enterobacter aerogenes*, *Klebsiella planticola* and *Serratia ficaria* and Determination of Nucleotide Sequences of the Genes

Chromosomal DNA was extracted from cultivated microbial cells of *Enterobacter aerogenes* IFO 12010, *Klebsiella planticola* IFO 14939 and *Serratia ficaria* IAM 13540 in accordance with a method of Murray and Thomson (Nucl. Acid Res., 4321, 8 (1980)). Then, in accordance with the method described in Example 7(2), a chromosomal gene expression library comprising about 20,000 transformants of *Escherichia coli* JM109 was constructed and screened to obtain transformants which showed transphosphorylation activity. It was considered that each of these transformants harbours the acid phosphatase gene derived from each of the original strains.

Plasmid DNA was extracted from one of the transformants of *Escherichia coli* which was considered to have the acid phosphatase gene derived from *Enterobacter aerogenes* IFO 12010 in accordance with an alkaline lysis method and the inserted DNA of the plasmid was analyzed. The above plasmid was designated as pENP100. A restriction enzyme map of the inserted DNA derived from *Enterobacter aerogenes* IFO 12010 is shown in Fig. 9.

As a result of specifying the region of acid phosphatase gene by subcloning, it was suggested that the acid phosphatase gene is contained in the 1.6 kbp fragment excised by restriction enzymes *Sall* and *Kpn*I. Then, the *Sall*-*Kpn*I fragment was ligated with pUC118 which was digested with *Sall* and *Kpn*I to construct a plasmid. The resulting plasmid was designated as pENP110.

According to the procedure as described above, plasmid DNA was extracted from one of the transformants of *Escherichia coli* which was considered to have the acid phosphatase gene derived from *Klebsiella planticola* IFO 14939 in accordance with an alkaline lysis method and the insert DNA of the plasmid was analyzed. The above plasmid was designated as pKLP100. A restriction enzyme map of the inserted DNA derived from *Klebsiella planticola* IFO 14939 is shown in Fig. 10.

As a result of specifying the region of acid phosphatase gene by subcloning, it was suggested that the acid phosphatase gene is contained in the 2.2 kbp fragment excised by restriction enzymes *Kpn*I and *Eco*RI. Then, the *Kpn*I-*Eco*RI fragment was ligated with pUC118 which was digested with *Kpn*I and *Eco*RI to construct a plasmid. The resulting plasmid was designated as pKLP110.

Similarly, plasmid DNA was extracted from one of the transformants of *Escherichia coli* which was considered to

have the acid phosphatase gene derived from *Serratia ficaria* IAM 13540 in accordance with an alkaline lysis method and the inserted DNA of the plasmid was analyzed. The above plasmid was designated as pSEP100. A restriction enzyme map of the inserted DNA derived from *Serratia ficaria* IAM 13540 is shown in Fig. 11.

As a result of specifying the region of acid phosphatase gene by subcloning, it was suggested that the acid phosphatase gene is contained in the 1.4 kbp fragment excised by restriction enzymes *Hind*III. Then, the *Hind*III fragment was ligated with pUC118 which was digested with *Hind*III to construct a plasmid. The resulting plasmid was designated as pSEP110.

Then, the plasmid DNAs were extracted from the transformants, *Escherichia coli* JM109/pENP110, *Escherichia coli* JM109/pKLP110 and *Escherichia coli* JM109/pSEP110, to which pENP110 pKLP110 and pSEP110 had been introduced, respectively, in accordance with an alkaline lysis method. The nucleotide sequences of inserts of these plasmids were determined in accordance with the method described in Example 8. The determined nucleotide sequences of open reading frames of the inserts are shown in SEQ ID NO: 23 for *Enterobacter aerogenes* IFO 12010, in SEQ ID NO: 25 for *Klebsiella planticola* IFO 14939 and in SEQ ID NO: 27 for *Serratia ficaria* IAM 13540. Additionally, the deduced amino acid sequences are shown in SEQ ID NOs: 24, 26 and 28, respectively. Because of the fact that the transformants harboring the plasmids containing these fragments exhibited the transphosphorylation activity, it was identified that these open reading frames were the objective acid phosphatase genes.

The nucleotide sequences and the deduced amino acid sequences were respectively compared with known sequences for homology. Data bases of EMBL and SWISS-PROT were used. As a result, it has been revealed that the genes illustrated in SEQ ID NO: 23, 25 and 27 in Sequence Listing are new genes. It is assumed that the protein encoded by the gene derived from *Enterobacter aerogenes* IFO 12010 comprises 248 amino acid residues, the protein encoded by the gene derived from *Klebsiella planticola* IFO 14939 comprises 248 amino acid residues and the protein encoded by the gene derived from *Serratia ficaria* IAM 13540 comprises 244 amino acid residues. There is a possibility that these proteins may be precursor proteins like the acid phosphatases derived from *Morganella morganii* and *Escherichia blattae*.

The amino acid sequences deduced from the nucleotide sequences are shown in Fig. 12 in one-letter together with the deduced amino acid sequence of the acid phosphatase derived from *Morganella morganii* NCIMB 10466 obtained in Example 8, that of *Escherichia blattae* JCM 1650 obtained in Example 12 and the known amino acid sequence of the acid phosphatase of *Providencia stuartii* (EMBL Accession number X64820). Common amino acid residues among all of the amino acids sequences are indicated with asterisks under the sequences in Fig. 12.

As shown in Fig. 12, the amino acid sequences of the acid phosphatases derived from six strains are highly homologous each other and 130 amino acid residues are common among all of the amino acid sequences. Thus, it is assumed that these acid phosphatases have similar functions.

Example 25: Amplification of Activity by Expressing Gene of Acid Phosphatase Derived from *Enterobacter aerogenes*, *Klebsiella planticola* and *Serratia ficaria*

Escherichia coli JM109/pPRP100 constructed in Example 23, *Escherichia coli* JM109/pENP110, *Escherichia coli* JM109/pKLP110 and *Escherichia coli* JM109/pSEP110 constructed in Example 24 were inoculated to an L-medium (50 ml) containing 100 µg/ml of ampicillin and 1 mM of IPTG, and were cultivated at 37 °C for 16 hours. Microbial cells were harvested from these cultures by centrifugation, and they were washed once with physiological saline. The microbial cells were suspended in 100 mM potassium phosphate buffer (5 ml, pH 7.0), and they were disrupted by means of a ultrasonic treatment performed at 4 °C for 20 minutes. The treated solutions were centrifuged to remove an insoluble fraction, and thus cell-free extracts were prepared.

The transphosphorylation activities of the obtained cell-free extracts were measured while using controls of cell-free extracts prepared from *Providencia stuartii* ATCC 29851, *Enterobacter aerogenes* IFO 12010, *Klebsiella planticola* IFO 14939, *Serratia ficaria* IAM 13450, and *Escherichia coli* JM109 transformed with the plasmid pUC118 in the same manner as described above. Results are shown in Table 16. The transphosphorylation activities were low in all of the wild type strains. The transphosphorylation activity was not detected in *Escherichia coli* JM109/pUC118. On the other hand, the transformants of *Escherichia coli* JM109 to which the acid phosphatase genes were introduced exhibited high transphosphorylation activities in comparison with wild type strains. According to the result, it has been demonstrated that each of the introduced DNA fragment allow *Escherichia coli* to express the acid phosphatase at a high level.

Table 16

Microbial strain	Transphosphorylation Activity (units/mg)
<i>Providencia stuartii</i> ATCC 29851	0.005
<i>Enterobacter aerogenes</i> IFO 12010	0.002

Table 16 (continued)

Microbial strain	Transphosphorylation Activity (units/mg)
<i>Klebsiella planticola</i> IFO 14939	0.002
<i>Serratia ficaria</i> IAM 13450	0.001
<i>Escherichia coli</i> JM109/pUC118	not detected
<i>Escherichia coli</i> JM109/pPRP100	0.833
<i>Escherichia coli</i> JM109/pENP110	0.301
<i>Escherichia coli</i> JM109/pKLP110	0.253
<i>Escherichia coli</i> JM109/pSEP110	0.123

Example 26**Production of a mutant acid phosphatase gene having an improved temperature stability:**

As described in Examples 20, 21 and 22, the *E. blattae*-derived mutant acid phosphatase gene-containing strain produced in Example 19 expressed the considerable amount of the acid phosphatase. In the production of 5'-inosinic acid from pyrophosphoric acid and inosine using this strain, 5'-inosinic acid was formed and accumulated in the high conversion yield. The optimum reaction temperature of this acid phosphatase was 35°C. However, when this reaction was conducted at a higher temperature, the reaction rate was increased, and the reaction was conducted upon increasing the nucleoside concentration of the phosphate acceptor in the reaction solution. Accordingly, it was expected that the nucleoside-5'-phosphate ester could be produced more efficiently for a shorter period of time. Thus, the temperature stability of the enzyme was improved upon introducing the mutation into the *E. blattae*-derived acid phosphatase gene cloned in Example 19 by the site specific mutation method using PCR.

Plasmid pEPI380 containing the gene encoding the *E. blattae* JCM1650-derived mutant acid phosphatase described in Example 19 was used, and the site specific mutation was introduced into this plasmid DNA by the genetic engineering method to produce the gene encoding the mutant acid phosphatase having the increased temperature stability. pEPI380 is a plasmid DNA obtained by binding a DNA fragment of 2.4 Kbp containing the gene encoding the mutant acid phosphatase derived from *E. blattae* JCM1650 and cleaved with restriction endonucleases C1al and BamHI to pBluescript KS(+) (supplied by Stratagene) cleaved with C1al and BamHI. The amino acid sequence of the mature protein anticipated from the base sequence of the gene encoding the acid phosphatase is presumed to be 11 amino acid residues shown in Table 12 in Example 19 in the sequence represented by SEQ ID NO: 8 in Sequence Listing.

Oligonucleotides MUT300 (SEQ ID NO: 9 in Sequence Listing), MUT400 (SEQ ID NO: 29 in Sequence Listing) and MUT410 (SEQ ID NO: 30 in Sequence Listing) having the sequences shown in Sequence Table were synthesized by the phosphoamidite method using a DNA synthesizer (Model 394 supplied by Applied Biosystem).

A mutant gene encoding a mutant phosphatase in which the 104th glutamic acid residue (GAG) of a maturation protein was substituted with a glycine residue (GG*T*) was produced by the method with PCR as in Example 15 using pEPI380 described in Example 19 as a template and MUT300 and MUT410 as primers for introduction of mutation. This mutant gene-containing plasmid was designated pEPI410. Likewise, a mutant gene encoding a mutant phosphatase in which the 151st threonine residue (ACC) was substituted with an alanine residue (G*CC) was produced using pEPI380 as a template and oligonucleotides MUT300, MUT310 and MUT420 as primers for introduction of mutation. This mutant gene-containing plasmid was designated pEPI420.

A plasmid was produced from the transformant of *E. coli* JM109 having introduced therein plasmids pEPI410 and pEPI420 containing the mutant phosphatase gene by the alkali bacteriolysis method, the base sequence was determined, and it was identified that the desired base was substituted.

Each of *E. coli* JM109/pEPI410 and *E. coli* JM109/pEPI420 having introduced therein the mutant acid phosphatase gene as produced in this Example and *E. coli* JM109/pEPI380 described in Example 19 was inoculated in 50 ml of an L medium containing 100 µg/ml of ampicillin and 1 mM of IPTG, and incubated at 37°C for 16 hours. The cells were collected from 50 ml of the culture solution of each of the strains, and washed once with a physiological saline solution. These cells were suspended in 5 ml of a 100-mM phosphate buffer (pH 7.0), and sonicated at 4°C for 20 minutes to mill the cells. The thus-treated solution was centrifuged to remove insoluble fractions and prepare a cell-free extract.

The cell-free extract formed from each of the strains was warmed at temperatures ranging from 0°C to 80°C with a pH of 7.0 for 30 minutes. After the completion of the warming, the transphosphorylation was conducted under the standard reaction conditions of pH of 4.0 and 30°C using the cell-free extracts treated at various temperatures, and the residual activity was measured. The results are shown in Fig. 13. The mutant enzyme expressed in *E. coli* JM109/pEPI380 described in Example 19 was stable in the treatment at 40°C for 30 minutes, but the decrease in the activity was observed at higher temperatures. By contrast, the new mutant enzyme expressed in *E. coli* JM109/pEPI410

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and E. coli JM109/pEPI420 having introduced therein the new mutant enzyme gene as produced in this Example improved the temperature stability, and the decrease in the activity was not observed even through the treatment at 50°C for 30 minutes. It was thus expected that when a nucleoside-5'-phosphate ester was produced using these strains at a high temperature, the productivity was further improved.

Example 27

Production of 5'-inosinic acid and 5'-guanylic acid using a mutant acid phosphatase gene-containing strain having an improved temperature stability:

Each of E. coli JM109/pEPI410 and E. coli JM109/pEPI420 having been introduced therein with the mutant acid phosphatase gene and E. coli JM109/pEPI380 described in Example 19 was inoculated in 50 ml of an L medium containing 100 µg/ml of ampicillin and 1 mM of IPTG, and incubated at 37°C for 16 hours.

Pyrophosphoric acid (15 g/dl) and 8 g/dl of inosine or guanosine were dissolved in an acetate buffer (pH 4.0). To this was added E. coli JM109 strain having introduced therein each mutant acid phosphatase gene such that the concentration reached 100 mg/dl in terms of the dry cell weight. The reaction was conducted at 50°C for 9 hours while maintaining the pH at 4.0, and the amount of 5'-inosinic acid or 5'-guanylic acid formed was measured. The results are shown in Table 17. The nucleoside phosphate ester formed was only a nucleoside-5'-phosphate ester, and the production of a nucleoside-2'-phosphate ester and a nucleoside-3'-phosphate ester as by-products was not observed at all. The reaction was also conducted at 35°C for 12 hours using E. coli JM109/pEPI380 strain as a control. The results are also shown in Table 17.

As described in Example 21, the nucleoside-5'-phosphate ester was formed and accumulated efficiently with E. coli JM109/pEPI380. By contrast, when the reaction was conducted using E. coli JM109/pEPI410 and E. coli JM109/pEPI420 having been introduced therein with the new mutant acid phosphatase gene derived from E. blattae as produced in Example 26, 5'-inosinic acid or 5'-guanylic acid in the same amount was formed and accumulated for a shorter period of time. Thus, the nucleoside-5'-phosphate ester could be produced more efficiently. Especially when using E. coli JM109/pEPI420, not only was the reaction time shortened, but also were 5'-inosinic acid and 5'-guanylic acid accumulated in larger amounts, and quite a high productivity was shown.

Table 17

Strain	Reaction temperature (°C)	Reaction time (hr)	Amount of 5'-inosine acid formed (g/dl)	Amount of 5'-guanylic acid formed (g/dl)
E. coli JM109/pEPI380	30	12	12.05	5.78
E. coli JM109/pEPI410	50	9	11.85	5.80
E. coli JM109/pEIP420	50	9	12.60	6.11

Annex to the description

SEQUENCE LISTING

5

INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) PROTEIN FRAGMENT TYPE: N-terminal
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Morganella morganii*
 (B) STRAIN: NCIMB 10466
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 Ala Ile Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro Asp Leu Tyr Tyr
 1 5 10 15
 Leu Lys Asn Glu
 20

20

INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 750 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Morganella morganii*
 (B) STRAIN: NCIMB 10466
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..747
 (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..60
 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 61..747
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 ATG AAG AAG AAT ATT ATC GCC GGT TGT CTG TTC TCA CTG TTT TCC CTT 48
 Met Lys Lys Asn Ile Ile Ala Gly Cys Leu Phe Ser Leu Phe Ser Leu
 -20 -15 -10 -5
 TCC GCG CTG GCC GCG ATC CCG GCG GGC AAC GAT GCC ACC ACC AAG CCG 96
 Ser Ala Leu Ala Ala Ile Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro
 1 5 10
 GAT TTA TAT TAT CTG AAA AAT GAA CAG GCT ATC GAC AGC CTG AAA CTG 144

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	Asp	Leu	Tyr	Tyr	Leu	Lys	Asn	Glu	Gln	Ala	Ile	Asp	Ser	Leu	Lys	Leu	
			15					20				25					
	TTA	CCG	CCA	CCG	CCG	GAA	GTC	GGC	AGT	ATT	CAG	TTT	TTA	AAT	GAT	CAG	192
5	Leu	Pro	Pro	Pro	Pro	Glu	Val	Gly	Ser	Ile	Gln	Phe	Leu	Asn	Asp	Gln	
		30					35				40						
	GCA	ATG	TAT	GAG	AAA	GGC	CGT	ATG	CTG	CGC	AAT	ACC	GAG	CGC	GGA	AAA	240
	Ala	Met	Tyr	Glu	Lys	Gly	Arg	Met	Leu	Arg	Asn	Thr	Glu	Arg	Gly	Lys	
		45				50				55						60	
10	CAG	GCA	CAG	GCA	GAT	GCT	GAC	CTG	GCC	GCA	GGG	GGT	GTG	GCA	ACC	GCA	288
	Gln	Ala	Gln	Ala	Asp	Ala	Asp	Leu	Ala	Ala	Gly	Gly	Val	Ala	Thr	Ala	
					65				70						75		
	TTT	TCA	GGG	GCA	TTC	GGC	TAT	CCG	ATA	ACC	GAA	AAA	GAC	TCT	CCG	GAG	336
15	Phe	Ser	Gly	Ala	Phe	Gly	Tyr	Pro	Ile	Thr	Glu	Lys	Asp	Ser	Pro	Glu	
			80					85				90					
	CTG	TAT	AAA	CTG	CTG	ACC	AAT	ATG	ATT	GAG	GAT	GCC	GGT	GAT	CTT	GCC	384
	Leu	Tyr	Lys	Leu	Leu	Thr	Asn	Met	Ile	Glu	Asp	Ala	Gly	Asp	Leu	Ala	
			95				100					105					
20	ACC	CGC	TCC	GCC	AAA	GAA	CAT	TAC	ATG	CGC	ATC	CGG	CCG	TTT	GCG	TTT	432
	Thr	Arg	Ser	Ala	Lys	Glu	His	Tyr	Met	Arg	Ile	Arg	Pro	Phe	Ala	Phe	
			110				115					120					
	TAC	GGC	ACA	GAA	ACC	TGT	AAT	ACC	AAA	GAT	CAG	AAA	AAA	CTC	TCC	ACC	480
	Tyr	Gly	Thr	Glu	Thr	Cys	Asn	Thr	Lys	Asp	Gln	Lys	Lys	Leu	Ser	Thr	
25		125				130				135					140		
	AAC	GGA	TCT	TAC	CCG	TCA	GGT	CAT	ACG	TCT	ATC	GGC	TGG	GCA	ACC	GCA	528
	Asn	Gly	Ser	Tyr	Pro	Ser	Gly	His	Thr	Ser	Ile	Gly	Trp	Ala	Thr	Ala	
					145				150						155		
	CTG	GTG	CTG	GCG	GAA	GTG	AAC	CCG	GCA	AAT	CAG	GAT	GCG	ATT	CTG	GAA	576
30	Leu	Val	Leu	Ala	Glu	Val	Asn	Pro	Ala	Asn	Gln	Asp	Ala	Ile	Leu	Glu	
					160				165						170		
	CGG	GGT	TAT	CAG	CTC	GGA	CAG	AGC	CGG	GTG	ATT	TGC	GGC	TAT	CAC	TGG	624
	Arg	Gly	Tyr	Gln	Leu	Gly	Gln	Ser	Arg	Val	Ile	Cys	Gly	Tyr	His	Trp	
			175				180					185					
35	CAG	AGT	GAT	GTG	GAT	GCC	GCG	CGG	ATT	GTC	GGT	TCA	GCC	GCT	GTC	GCG	672
	Gln	Ser	Asp	Val	Asp	Ala	Ala	Arg	Ile	Val	Gly	Ser	Ala	Ala	Val	Ala	
			190				195					200					
	ACA	TTA	CAT	TCC	GAT	CCG	GCA	TTT	CAG	GCG	CAG	TTA	GCG	AAA	GCC	AAA	720
	Thr	Leu	His	Ser	Asp	Pro	Ala	Phe	Gln	Ala	Gln	Leu	Ala	Lys	Ala	Lys	
40		205				210				215					220		
	CAG	GAA	TTT	GCA	CAA	AAA	TCA	CAG	AAA	TAA							750
	Gln	Glu	Phe	Ala	Gln	Lys	Ser	Gln	Lys								
					225				229								

45 INFORMATION FOR SEQ ID NO:3:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 amino acids
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Morganella morganii*
(B) STRAIN: NCIMB 10466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

10 Met Lys Lys Asn Ile Ile Ala Gly Cys Leu Phe Ser Leu Phe Ser Leu
   -20               -15               -10               -5
   Ser Ala Leu Ala Ala Ile Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro
                        1               5               10
15 Asp Leu Tyr Tyr Leu Lys Asn Glu Gln Ala Ile Asp Ser Leu Lys Leu
   15               20               25
   Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Gln Phe Leu Asn Asp Gln
   30               35               40
   Ala Met Tyr Glu Lys Gly Arg Met Leu Arg Asn Thr Glu Arg Gly Lys
20 45               50               55               60
   Gln Ala Gln Ala Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Thr Ala
                        65               70               75
   Phe Ser Gly Ala Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ser Pro Glu
25 80               85               90
   Leu Tyr Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
   95               100              105
   Thr Arg Ser Ala Lys Glu His Tyr Met Arg Ile Arg Pro Phe Ala Phe
   110              115              120
30 Tyr Gly Thr Glu Thr Cys Asn Thr Lys Asp Gln Lys Lys Leu Ser Thr
   125              130              135              140
   Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
                        145              150              155
35 Leu Val Leu Ala Glu Val Asn Pro Ala Asn Gln Asp Ala Ile Leu Glu
   160              165              170
   Arg Gly Tyr Gln Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
   175              180              185
   Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Ala Val Ala
40 190              195              200
   Thr Leu His Ser Asp Pro Ala Phe Gln Ala Gln Leu Ala Lys Ala Lys
   205              210              215              220
   Gln Glu Phe Ala Gln Lys Ser Gln Lys
45 225              229

```

INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Morganella morganii*

(B) STRAIN: NCIMB 10466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

5   Ala Ile Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro Asp Leu Tyr Tyr
    1           5           10           15
    Leu Lys Asn Glu Gln Ala Ile Asp Ser Leu Lys Leu Leu Pro Pro Pro
      20           25           30
10  Pro Glu Val Gly Ser Ile Gln Phe Leu Asn Asp Gln Ala Met Tyr Glu
    35           40           45
    Lys Gly Arg Met Leu Arg Asn Thr Glu Arg Gly Lys Gln Ala Gln Ala
    50           55           60
15  Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Thr Ala Phe Ser Gly Ala
    65           70           75           80
    Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ser Pro Glu Leu Tyr Lys Leu
      85           90           95
    Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala Thr Arg Ser Ala
    100          105          110
    Lys Glu His Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Gly Thr Glu
    115          120          125
    Thr Cys Asn Thr Lys Asp Gln Lys Lys Leu Ser Thr Asn Gly Ser Tyr
    130          135          140
25  Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala Leu Val Leu Ala
    145          150          155          160
    Glu Val Asn Pro Ala Asn Gln Asp Ala Ile Leu Glu Arg Gly Tyr Gln
      165          170          175
30  Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser Asp Val
    180          185          190
    Asp Ala Ala Arg Ile Val Gly Ser Ala Ala Val Ala Thr Leu His Ser
    195          200          205
35  Asp Pro Ala Phe Gln Ala Gln Leu Ala Lys Ala Lys Gln Glu Phe Ala
    210          215          220
    Gln Lys Ser Gln Lys
    225          229

```

40 INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) PROTEIN FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: *Escherichia blattae*

(B) STRAIN: JCM 1650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Leu Ala Leu Val Ala Thr Gly Asn Asp Thr Thr Thr Lys Pro Asp Leu
1           5           10           15

```

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INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia blattae*

(B) STRAIN: JCM 1650

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..747

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..54

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 55..747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25	ATG AAA AAA CGT GTT CTG GCA GTT TGT TTT GCC GCA TTG TTC TCT TCT	48
	Met Lys Lys Arg Val Leu Ala Val Cys Phe Ala Ala Leu Phe Ser Ser	
	-18 -15 -10 -5	
	CAG GCC CTG GCG CTG GTC GCT ACC GGC AAC GAC ACT ACC ACG AAA CCG	96
	Gln Ala Leu Ala Leu Val Ala Thr Gly Asn Asp Thr Thr Lys Pro	
	1 5 10	
30	GAT CTC TAC TAC CTC AAG AAC AGT GAA GCC ATT AAC AGC CTG GCG CTG	144
	Asp Leu Tyr Tyr Leu Lys Asn Ser Glu Ala Ile Asn Ser Leu Ala Leu	
	15 20 25 30	
	TTG CCG CCA CCA CCG GCG GTG GGC TCC ATT GCG TTT CTC AAC GAT CAG	192
	Leu Pro Pro Pro Pro Ala Val Gly Ser Ile Ala Phe Leu Asn Asp Gln	
35	35 40 45	
	GCC ATG TAT GAA CAG GGG CGC CTG CTG CGC AAC ACC GAA CGC GGT AAG	240
	Ala Met Tyr Glu Gln Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys	
	50 55 60	
40	CTG GCG GCG GAA GAT GCA AAC CTG AGC AGT GGC GGG GTG GCG AAT GCT	288
	Leu Ala Ala Glu Asp Ala Asn Leu Ser Ser Gly Gly Val Ala Asn Ala	
	65 70 75	
	TTC TCC GGC GCG TTT GGT AGC CCG ATC ACC GAA AAA GAC GCC CCG GCG	336
	Phe Ser Gly Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Ala	
	80 85 90	
45	CTG CAT AAA TTA CTG ACC AAT ATG ATT GAG GAC GCC GGG GAT CTG GCG	384
	Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala	
	95 100 105 110	
50	ACC CGC AGC GCG AAA GAT CAC TAT ATG CGC ATT CGT CCG TTC GCG TTT	432

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	Thr	Arg	Ser	Ala	Lys	Asp	His	Tyr	Met	Arg	Ile	Arg	Pro	Phe	Ala	Phe	
					115					120					125		
	TAT	GGG	GTC	TCT	ACC	TGT	AAT	ACC	ACC	GAG	CAG	GAC	AAA	CTG	TCC	AAA	480
5	Tyr	Gly	Val	Ser	Thr	Cys	Asn	Thr	Thr	Glu	Gln	Asp	Lys	Leu	Ser	Lys	
				130					135					140			
	AAT	GGC	TCT	TAT	CCG	TCC	GGG	CAT	ACC	TCT	ATC	GGC	TGG	GCT	ACT	GCG	528
	Asn	Gly	Ser	Tyr	Pro	Ser	Gly	His	Thr	Ser	Ile	Gly	Trp	Ala	Thr	Ala	
			145					150					155				
10	CTG	GTG	CTG	GCA	GAG	ATC	AAC	CCT	CAG	CGC	CAG	AAC	GAG	ATC	CTG	AAA	576
	Leu	Val	Leu	Ala	Glu	Ile	Asn	Pro	Gln	Arg	Gln	Asn	Glu	Ile	Leu	Lys	
		160					165					170					
	CGC	GGT	TAT	GAG	CTG	GGC	CAG	AGC	CGG	GTG	ATT	TGC	GGC	TAC	CAC	TGG	624
15	Arg	Gly	Tyr	Glu	Leu	Gly	Gln	Ser	Arg	Val	Ile	Cys	Gly	Tyr	His	Trp	
	175					180					185					190	
	CAG	AGT	GAT	GTG	GAT	GCC	GCG	CGG	GTA	GTG	GGA	TCT	GCC	GTT	GTG	GCG	672
	Gln	Ser	Asp	Val	Asp	Ala	Ala	Arg	Val	Val	Gly	Ser	Ala	Val	Val	Ala	
					195					200					205		
20	ACC	CTG	CAT	ACC	AAC	CCG	GCG	TTC	CAG	CAG	CAG	TTG	CAG	AAA	GCG	AAG	720
	Thr	Leu	His	Thr	Asn	Pro	Ala	Phe	Gln	Gln	Gln	Leu	Gln	Lys	Ala	Lys	
					210				215					220			
	GCC	GAA	TTC	GCC	CAG	CAT	CAG	AAG	AAA	TAA							750
	Ala	Glu	Phe	Ala	Gln	His	Gln	Lys	Lys								
25			225						230								

INFORMATION FOR SEQ ID NO:7:

	(i) SEQUENCE CHARACTERISTICS:																
	(A) LENGTH: 249 amino acids																
30	(B) TYPE: amino acid																
	(D) TOPOLOGY: linear																
	(ii) MOLECULE TYPE: protein																
	(vi) ORIGINAL SOURCE:																
	(A) ORGANISM: Escherichia blattae																
35	(B) STRAIN: JCM 1650																
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:																
	Met	Lys	Lys	Arg	Val	Leu	Ala	Val	Cys	Phe	Ala	Ala	Leu	Phe	Ser	Ser	
	-18		-15					-10					-5				
40	Gln	Ala	Leu	Ala	Leu	Val	Ala	Thr	Gly	Asn	Asp	Thr	Thr	Thr	Lys	Pro	
		1			5							10					
	Asp	Leu	Tyr	Tyr	Leu	Lys	Asn	Ser	Glu	Ala	Ile	Asn	Ser	Leu	Ala	Leu	
	15				20					25						30	
	Leu	Pro	Pro	Pro	Pro	Ala	Val	Gly	Ser	Ile	Ala	Phe	Leu	Asn	Asp	Gln	
					35				40					45			
45	Ala	Met	Tyr	Glu	Gln	Gly	Arg	Leu	Leu	Arg	Asn	Thr	Glu	Arg	Gly	Lys	
			50					55					60				
	Leu	Ala	Ala	Glu	Asp	Ala	Asn	Leu	Ser	Ser	Gly	Gly	Val	Ala	Asn	Ala	
			65					70					75				

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Phe Ser Gly Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Ala
 80 85 90
 5 Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
 95 100 105 110
 Thr Arg Ser Ala Lys Asp His Tyr Met Arg Ile Arg Pro Phe Ala Phe
 115 120 125
 10 Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys
 130 135 140
 Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
 145 150 155
 15 Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
 160 165 170
 Arg Gly Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
 175 180 185 190
 20 Gln Ser Asp Val Asp Ala Ala Arg Val Val Gly Ser Ala Val Val Ala
 195 200 205
 Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
 210 215 220
 Ala Glu Phe Ala Gln His Gln Lys Lys
 225 230
 25

INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Escherichia blattae
 (B) STRAIN: JCM 1650
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
 Leu Ala Leu Val Ala Thr Gly Asn Asp Thr Thr Thr Lys Pro Asp Leu
 1 5 10 15
 40 Tyr Tyr Leu Lys Asn Ser Glu Ala Ile Asn Ser Leu Ala Leu Leu Pro
 20 25 30
 Pro Pro Pro Ala Val Gly Ser Ile Ala Phe Leu Asn Asp Gln Ala Met
 35 40 45
 45 Tyr Glu Gln Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys Leu Ala
 50 55 60
 Ala Glu Asp Ala Asn Leu Ser Ser Gly Gly Val Ala Asn Ala Phe Ser
 65 70 75 80
 50 Gly Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Ala Leu His
 85 90 95
 Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala Thr Arg
 100 105 110
 55 Ser Ala Lys Asp His Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Gly

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      115      120      125
Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys Asn Gly
      130      135      140
5  Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala Leu Val
      145      150      155      160
Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys Arg Gly
      165      170      175
Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser
      180      185      190
10 Asp Val Asp Ala Ala Arg Val Val Gly Ser Ala Val Val Ala Thr Leu
      195      200      205
His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys Ala Glu
      210      215      220
15 Phe Ala Gln His Gln Lys Lys
      225      230

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INFORMATION FOR SEQ ID NO:9:

```

      20  (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 20 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
      25  (ii) MOLECULE TYPE: other DNA..synthetic DNA
      (iii) HYPOTHETICAL: NO
      (iv) ANTI-SENSE: NO
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
CCTCGAGGTC GACGGTATCG

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INFORMATION FOR SEQ ID NO:10:

```

      30  (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
      35  (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: other DNA..synthetic DNA
      (iii) HYPOTHETICAL: NO
          (iv) ANTI-SENSE: YES
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
      40  ATTCGCCACA TCGCCACTGC T

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21

INFORMATION FOR SEQ ID NO:11:

```

      45  (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 22 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
      50  (ii) MOLECULE TYPE: other DNA..synthetic DNA

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(iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
 5 TAGCCCAGCC GGTAGAGGTA TG 22

INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 15 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
 TGCATCTGCC TGCGCCTGCT TAC 23

INFORMATION FOR SEQ ID NO:13:
 (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
 30 AACGCGCCGT AGAAAGCATT 20

INFORMATION FOR SEQ ID NO:14:
 (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 40 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
 GTCCTGGTCT TTGGIATTAC A 21

INFORMATION FOR SEQ ID NO:15:
 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 50 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
 CACATCGCCA GCGGCCAGGT CTGCAT 26

INFORMATION FOR SEQ ID NO:16:
 (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 15 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
 GCATATAGTG TTCTTTCGCG C 21

20 INFORMATION FOR SEQ ID NO:17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
 30 ATTACAGGTT TCGACCCCAT AA 22

INFORMATION FOR SEQ ID NO:18:
 (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 40 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
 TGATGCATGT CCGGGCTGTC TTTT 25

45 INFORMATION FOR SEQ ID NO:19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 50 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: YES
 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
 CTGGATCCTG TGGCTATCAT CACCT 25

INFORMATION FOR SEQ ID NO:20:
 (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 15 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
 CTGGATCCGA CGCGATTTTA CCATA 25

INFORMATION FOR SEQ ID NO:21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 747 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: Providencia stuartii
 (B) STRAIN: ATCC 29851
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..744
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
 ATG AAA AAA CTA TTA GCA GTA TTC TGC GCA GGG GCT TTT GTT TCA ACC 48
 Met Lys Lys Leu Leu Ala Val Phe Cys Ala Gly Ala Phe Val Ser Thr
 1 5 10 15
 40 AGT GTA TTT GCG GCG ATC CCT CCC GGC AAT GAT GTG ACA ACT AAA CCC 96
 Ser. Val Phe Ala Ala Ile Pro Pro Gly Asn Asp Val Thr Thr Lys Pro
 20 25 30
 GAT CTT TAT TAT TTA AAA AAC TCA CAG GCT ATT GAT AGT TTA GCG TTA 144
 Asp Leu Tyr Tyr Leu Lys Asn Ser Gln Ala Ile Asp Ser Leu Ala Leu
 35 40 45
 45 TTG CCG CCA CCA CCT GAA GTG GGC AGT ATC TTA TTT TTA AAC GAC CAA 192
 Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Leu Phe Leu Asn Asp Gln
 50 55 60
 GCG ATG TAT GAA AAA GGC CGT TTA TTG CGA AAT ACT GAG CGT GGA GAA 240
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	Ala	Met	Tyr	Glu	Lys	Gly	Arg	Leu	Leu	Arg	Asn	Thr	Glu	Arg	Gly	Glu	
	65					70					75					80	
5	CAA	GCC	GCT	AAG	GAT	GCT	GAT	CTG	GCT	GCG	GGC	GGT	GTT	GCG	AAC	GCA	288
	Gln	Ala	Ala	Lys	Asp	Ala	Asp	Leu	Ala	Ala	Gly	Gly	Val	Ala	Asn	Ala	
				85						90					95		
	TTT	TCT	GAA	GCT	TTT	GGT	TAT	CCC	ATT	ACC	GAA	AAG	GAT	GCG	CCT	GAA	336
	Phe	Ser	Glu	Ala	Phe	Gly	Tyr	Pro	Ile	Thr	Glu	Lys	Asp	Ala	Pro	Glu	
				100					105					110			
10	ATT	CAT	AAA	TTG	CTG	ACG	AAT	ATG	ATT	GAA	GAT	GCG	GGG	GAT	TTA	GCA	384
	Ile	His	Lys	Leu	Leu	Thr	Asn	Met	Ile	Glu	Asp	Ala	Gly	Asp	Leu	Ala	
				115				120					125				
	ACT	CGC	TCA	GCC	AAA	GAG	AAA	TAC	ATG	CGC	ATT	CGT	CCA	TTT	GCG	TTC	432
15	Thr	Arg	Ser	Ala	Lys	Glu	Lys	Tyr	Met	Arg	Ile	Arg	Pro	Phe	Ala	Phe	
				130				135				140					
	TAC	GGT	GTT	GCT	ACC	TGT	AAC	ACG	AAA	GAT	CAG	GAC	AAA	TTA	TCT	AAG	480
	Tyr	Gly	Val	Ala	Thr	Cys	Asn	Thr	Lys	Asp	Gln	Asp	Lys	Leu	Ser	Lys	
				145		150				155				160			
20	AAT	GGC	TCT	TAT	CCT	TCT	GGA	CAC	ACC	GCA	ATT	GGC	TGG	GCA	TCT	GCA	528
	Asn	Gly	Ser	Tyr	Pro	Ser	Gly	His	Thr	Ala	Ile	Gly	Trp	Ala	Ser	Ala	
				165					170					175			
	CTC	GTA	TTG	TCA	GAA	ATT	AAC	CCA	GAA	AAC	CAA	GAT	AAA	ATT	TTA	AAA	576
	Leu	Val	Leu	Ser	Glu	Ile	Asn	Pro	Glu	Asn	Gln	Asp	Lys	Ile	Leu	Lys	
25				180					185				190				
	CGT	GGT	TAT	GAA	CTT	GGC	CAA	AGC	CGA	GTC	ATC	TGT	GGT	TAC	CAT	TGG	624
	Arg	Gly	Tyr	Glu	Leu	Gly	Gln	Ser	Arg	Val	Ile	Cys	Gly	Tyr	His	Trp	
				195				200					205				
	CAA	AGT	GAT	GTT	GAT	GCA	GCT	CGT	ATC	GTT	GCA	TCG	GGT	GCG	GTA	GCA	672
30	Gln	Ser	Asp	Val	Asp	Ala	Ala	Arg	Ile	Val	Ala	Ser	Gly	Ala	Val	Ala	
				210			215					220					
	ACT	TTA	CAC	TCC	AAC	CCT	GAA	TTC	CAA	AAA	CAG	TTA	CAA	AAA	GCC	AAA	720
	Thr	Leu	His	Ser	Asn	Pro	Glu	Phe	Gln	Lys	Gln	Leu	Gln	Lys	Ala	Lys	
				225		230				235					240		
35	GAC	GAA	TTT	GCT	AAA	CTG	AAA	AAA	TAG								747
	Asp	Glu	Phe	Ala	Lys	Leu	Lys	Lys									
				245													

INFORMATION FOR SEQ ID NO:22:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 248 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: protein
45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: Providencia stuartii
	(B) STRAIN: ATCC 29851
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
50	Met Lys Lys Leu Leu Ala Val Phe Cys Ala Gly Ala Phe Val Ser Thr

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      1           5           10           15
Ser Val Phe Ala Ala Ile Pro Pro Gly Asn Asp Val Thr Thr Lys Pro
      20           25           30
5  Asp Leu Tyr Tyr Leu Lys Asn Ser Gln Ala Ile Asp Ser Leu Ala Leu
      35           40           45
Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Leu Phe Leu Asn Asp Gln
      50           55           60
10 Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Glu
      65           70           75           80
Gln Ala Ala Lys Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Asn Ala
      85           90           95
15 Phe Ser Glu Ala Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ala Pro Glu
      100           105           110
Ile His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
      115           120           125
Thr Arg Ser Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe
20      130           135           140
Tyr Gly Val Ala Thr Cys Asn Thr Lys Asp Gln Asp Lys Leu Ser Lys
      145           150           155           160
Asn Gly Ser Tyr Pro Ser Gly His Thr Ala Ile Gly Trp Ala Ser Ala
      165           170           175
25 Leu Val Leu Ser Glu Ile Asn Pro Glu Asn Gln Asp Lys Ile Leu Lys
      180           185           190
Arg Gly Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
      195           200           205
30 Gln Ser Asp Val Asp Ala Ala Arg Ile Val Ala Ser Gly Ala Val Ala
      210           215           220
Thr Leu His Ser Asn Pro Glu Phe Gln Lys Gln Leu Gln Lys Ala Lys
      225           230           235           240
35 Asp Glu Phe Ala Lys Leu Lys Lys
      245

```

INFORMATION FOR SEQ ID NO:23:

```

      40 (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 744 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
      45 (ii) MOLECULE TYPE: genomic DNA
      46 (iii) HYPOTHETICAL: NO
          (iv) ANTI-SENSE: NO
          (vi) ORIGINAL SOURCE:
      50          (A) ORGANISM: Enterobacter aerogenes
          (B) STRAIN: IFO 12010
          (ix) FEATURE:
              (A) NAME/KEY: CDS
              (B) LOCATION: 1..744
      55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

	ATG	AAA	AAG	CGC	GTT	CTC	GCC	CTC	TGC	CTC	GCC	AGC	CTG	TTT	TCC	GTT	48
	Met	Lys	Lys	Arg	Val	Leu	Ala	Leu	Cys	Leu	Ala	Ser	Leu	Phe	Ser	Val	
5	1				5				10					15			
	AAC	GCT	TTC	GCG	CTG	GTC	CCT	GCC	GGC	AAT	GAT	GCA	ACC	ACC	AAA	CCG	96
	Asn	Ala	Phe	Ala	Leu	Val	Pro	Ala	Gly	Asn	Asp	Ala	Thr	Thr	Lys	Pro	
				20					25					30			
	GAT	CTC	TAT	TAT	CTG	AAA	AAT	GCA	CAG	GCC	ATC	GAT	AGT	CTG	GCG	CTG	144
10	Asp	Leu	Tyr	Tyr	Leu	Lys	Asn	Ala	Gln	Ala	Ile	Asp	Ser	Leu	Ala	Leu	
				35				40					45				
	TTG	CCG	CCG	CCG	CCG	GAA	GTT	GGC	AGC	ATC	GCA	TTT	TTA	AAC	GAT	CAG	192
	Leu	Pro	Pro	Pro	Glu	Val	Gly	Ser	Ile	Ala	Phe	Leu	Asn	Asp	Gln		
				50			55					60					
15	GCG	ATG	TAT	GAG	AAA	GGA	CGG	CTG	TTG	CGC	AAT	ACC	GAA	CGT	GGC	AAG	240
	Ala	Met	Tyr	Glu	Lys	Gly	Arg	Leu	Leu	Arg	Asn	Thr	Glu	Arg	Gly	Lys	
				65		70				75				80			
	CTG	GCG	GCT	GAA	GAT	GCT	AAC	CTG	AGC	GCC	GGC	GGC	GTC	GCG	AAT	GCC	288
	Leu	Ala	Ala	Glu	Asp	Ala	Asn	Leu	Ser	Ala	Gly	Gly	Val	Ala	Asn	Ala	
20				85						90				95			
	TTC	TCC	AGC	GCT	TTT	GGT	TCG	CCC	ATC	ACC	GAA	AAA	GAC	GCG	CCG	CAG	336
	Phe	Ser	Ser	Ala	Phe	Gly	Ser	Pro	Ile	Thr	Glu	Lys	Asp	Ala	Pro	Gln	
				100					105				110				
	TTA	CAT	AAG	CTG	CTG	ACA	AAT	ATG	ATT	GAG	GAT	GCC	GGC	GAT	CTG	GCC	384
25	Leu	His	Lys	Leu	Leu	Thr	Asn	Met	Ile	Glu	Asp	Ala	Gly	Asp	Leu	Ala	
				115			120					125					
	ACC	CGC	AGC	GCG	AAA	GAG	AAA	TAT	ATG	CGC	ATT	CGC	CCG	TTT	GCG	TTC	432
	Thr	Arg	Ser	Ala	Lys	Glu	Lys	Tyr	Met	Arg	Ile	Arg	Pro	Phe	Ala	Phe	
				130			135					140					
30	TAC	GGC	GTT	TCA	ACC	TGT	AAC	ACT	ACC	GAG	CAG	GAC	AAG	CTG	TCG	AAA	480
	Tyr	Gly	Val	Ser	Thr	Cys	Asn	Thr	Thr	Glu	Gln	Asp	Lys	Leu	Ser	Lys	
	145					150				155				160			
	AAC	GGA	TCT	TAC	CCT	TCC	GGC	CAT	ACC	TCT	ATC	GGT	TGG	GCA	ACC	GCG	528
35	Asn	Gly	Ser	Tyr	Pro	Ser	Gly	His	Thr	Ser	Ile	Gly	Trp	Ala	Thr	Ala	
				165						170				175			
	CTG	GTA	CTG	GCG	GAG	ATC	AAT	CCG	CAG	CGG	CAA	AAC	GAA	ATT	CTC	AAA	576
	Leu	Val	Leu	Ala	Glu	Ile	Asn	Pro	Gln	Arg	Gln	Asn	Glu	Ile	Leu	Lys	
				180					185				190				
40	CGC	GGC	TAT	GAA	TTG	GGC	GAA	AGC	CGG	GTT	ATC	TGC	GGC	TAT	CAT	TGG	624
	Arg	Gly	Tyr	Glu	Leu	Gly	Glu	Ser	Arg	Val	Ile	Cys	Gly	Tyr	His	Trp	
				195			200					205					
	CAG	AGC	GAT	GTC	GAT	GCG	GCG	CGG	ATA	GTC	GGC	TCG	GCG	GTG	GTG	GCG	672
	Gln	Ser	Asp	Val	Asp	Ala	Ala	Arg	Ile	Val	Gly	Ser	Ala	Val	Val	Ala	
45				210			215					220					
	ACC	CTG	CAT	ACC	AAC	CCG	GCC	TTC	CAA	CAG	CAG	TTG	CAG	AAA	GCA	AAG	720
	Thr	Leu	His	Thr	Asn	Pro	Ala	Phe	Gln	Gln	Gln	Leu	Gln	Lys	Ala	Lys	
						230					235					240	

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GAT GAA TTC GCC AAA ACG CAG AAG TAA
 Asp Glu Phe Ala Lys Thr Gln Lys
 245

747

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INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Enterobacter aerogenes

(B) STRAIN: IFO 12010

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Lys Lys Arg Val Leu Ala Leu Cys Leu Ala Ser Leu Phe Ser Val
 1 5 10 15
 Asn Ala Phe Ala Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro
 20 25 30
 Asp Leu Tyr Tyr Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu
 35 40 45
 Leu Pro Pro Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln
 50 55 60
 Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys
 25 65 70 75 80
 Leu Ala Ala Glu Asp Ala Asn Leu Ser Ala Gly Gly Val Ala Asn Ala
 85 90 95
 Phe Ser Ser Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Gln
 100 105 110
 Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
 30 115 120 125
 Thr Arg Ser Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe
 130 135 140
 Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys
 35 145 150 155 160
 Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
 165 170 175
 Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
 180 185 190
 Arg Gly Tyr Glu Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp
 40 195 200 205
 Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala
 210 215 220
 Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
 45 225 230 235 240
 Asp Glu Phe Ala Lys Thr Gln Lys
 245

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INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: IFO 14939

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG AAA AAG CGT GTA CTC GCC CTT TGC CTT GCC AGC CTC TTT TCA GTT	48
Met Lys Lys Arg Val Leu Ala Leu Cys Leu Ala Ser Leu Phe Ser Val	
1 5 10 15	
AGC GCC TTT GCG CTG GTT CCC GCC GGC AAT GAT GCC ACC ACC AAG CCC	96
Ser Ala Phe Ala Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro	
20 25 30	
GAT CTC TAC TAT CTG AAA AAT GCC CAG GCC ATT GAC AGC CTG GCG CTG	144
Asp Leu Tyr Tyr Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu	
35 40 45	
TTG CCA CCG CCG CCG GAA GTG GGC AGC ATT GCG TTT TTA AAC GAT CAG	192
Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln	
50 55 60	
GCG ATG TAT GAG AAA GGC CGT CTG CTG CGC GCC ACC GCC CGC GGC AAG	240
Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Ala Thr Ala Arg Gly Lys	
65 70 75 80	
TTG GCG GCA GAA GAT GCC AAC CTG AGC GCG GGT GGC GTG GCC AAC GCC	288
Leu Ala Ala Glu Asp Ala Asn Leu Ser Ala Gly Gly Val Ala Asn Ala	
85 90 95	
TTC TCC GCA GCA TTC GGC TCC CCG ATC AGC GAA AAA GAC GCC CCG GCG	336
Phe Ser Ala Ala Phe Gly Ser Pro Ile Ser Glu Lys Asp Ala Pro Ala	
100 105 110	
CTG CAC AAA CTG CTC ACC AAC ATG ATT GAA GAC GCG GGC GAT CTG GCG	384
Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala	
115 120 125	
ACC CGA GGC GCG AAA GAG AAG TAT ATG CGT ATT CGT CCG TTT GCC TTC	432
Thr Arg Gly Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe	
130 135 140	
TAC GGC GTG TCC ACC TGC AAT ACC ACC GAA CAG GAT AAG CTG TCG AAA	480
Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys	

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145		150		155		160	
AAC GGC TCC TAC CCT TCC GGA CAC ACC TCT ATC GGC TGG GCG ACC GCC							528
Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala							
	165		170		175		
CTG GTG CTG GCC GAA ATC AAC CCG CAG CGC CAG AAT GAG ATT CTC AAG							576
Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys							
	180		185		190		
CGC GGC TAT GAG CTC GGT GAA AGT CGG GTG ATC TGC GGT TAC CAC TGG							624
Arg Gly Tyr Glu Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp							
	195		200		205		
CAG AGC GAT GTT GAC GCC GCG CGG ATT GTC GGC TCG GCG GTG GTT GCA							672
Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala							
	210		215		220		
ACC CTG CAT ACC AAT CCG GCC TTC CAG CAG CAG CTG CAA AAA GCC AAA							720
Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys							
	225		230		235		240
GAC GAG TTT GCG AAA CAG CAG AAA TAG							747
Asp Glu Phe Ala Lys Gln Gln Lys							
	245						

INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: IFO 14939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Lys Lys Arg Val Leu Ala Leu Cys Leu Ala Ser Leu Phe Ser Val	
1 5 10 15	
Ser Ala Phe Ala Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro	
20 25 30	
Asp Leu Tyr Tyr Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu	
35 40 45	
Leu Pro Pro Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln	
50 55 60	
Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Ala Thr Ala Arg Gly Lys	
65 70 75 80	
Leu Ala Ala Glu Asp Ala Asn Leu Ser Ala Gly Gly Val Ala Asn Ala	
85 90 95	
Phe Ser Ala Ala Phe Gly Ser Pro Ile Ser Glu Lys Asp Ala Pro Ala	
100 105 110	
Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala	
115 120 125	
Thr Arg Gly Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe	

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130 135 140
Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys
145 150 155 160
5 Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
165 170 175
Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
180 185 190
Arg Gly Tyr Glu Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp
10 195 200 205
Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala
210 215 220
Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
225 230 235 240
15 Asp Glu Phe Ala Lys Gln Gln Lys
245

INFORMATION FOR SEQ ID NO:27:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 735 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
25 (ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia ficaria*
30 (B) STRAIN: IAM 13540
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
35 ATG AAA AAA ATA TTA TTA GCC ACA TTA AGC TGC GCC GCG TTG ACG CAG 48
Met Lys Lys Ile Leu Leu Ala Thr Leu Ser Cys Ala Ala Leu Thr Gln
1 5 10 15
TTT TCC TTT GCC GCC AAA GAT GTC ACT ACC CAC CCT GAG GTT TAT TTT 96
Phe Ser Phe Ala Ala Lys Asp Val Thr Thr His Pro Glu Val Tyr Phe
20 25 30
40 CTG CAA GAA TCA CAG TCC ATC GAC AGC CTG GCA CTA TTG CCG CCG CCG 144
Leu Gln Glu Ser Gln Ser Ile Asp Ser Leu Ala Leu Leu Pro Pro Pro
35 40 45
CCG GCG ATG GAC AGC ATT GAT TTC CTG AAT GAC AAA GCG CAA TAC GAC 192
Pro Ala Met Asp Ser Ile Asp Phe Leu Asn Asp Lys Ala Gln Tyr Asp
50 55 60
GCC GGG AAA ATA GTG CGC AAT ACT CCG CGT GGC AAG CAG GCT TAT GAT 240
Ala Gly Lys Ile Val Arg Asn Thr Pro Arg Gly Lys Gln Ala Tyr Asp

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	65		70		75		80	
	GAC	GCC	CAC	GTT	GCC	GGG	GAC	GGC
	Asp	Ala	His	Val	Ala	Gly	Asp	Gly
5	TTC	GGC	CTA	GAA	ATA	GCC	CAA	CGG
	Phe	Gly	Leu	Glu	Ile	Ala	Gln	Arg
	GTG	ATG	AAA	ATG	CGT	GAA	GAC	GCC
10	Val	Met	Lys	Met	Arg	Glu	Asp	Ala
	AAA	AAT	CAC	TAT	ATG	CGC	ATT	CGC
	Lys	Asn	His	Tyr	Met	Arg	Ile	Arg
15	ACC	TGC	CGA	CCG	GAC	GAA	GAA	AGC
	Thr	Cys	Arg	Pro	Asp	Glu	Ser	Thr
	CCT	TCC	GGC	CAT	ACC	ACC	ATC	GGC
20	Pro	Ser	Gly	His	Thr	Thr	Ile	Gly
	GAA	ATC	AAC	CCC	GCC	AGG	CAG	GGT
25	Glu	Ile	Asn	Pro	Ala	Arg	Gln	Gly
	ATG	GGC	CAA	AGC	CGG	GTT	ATC	TGC
	Met	Gly	Gln	Ser	Arg	Val	Ile	Cys
	ACT	GCG	GCG	CGC	ATG	GCG	GCG	TCG
30	Thr	Ala	Ala	Arg	Met	Ala	Ala	Ser
	GAA	CCC	ACC	TTC	GCC	GCC	CAG	CTG
	Glu	Pro	Thr	Phe	Ala	Ala	Gln	Leu
35	GGC	CTG	AAA	AAG	TAA			
	Gly	Leu	Lys	Lys				

INFORMATION FOR SEQ ID NO:28:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 244 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: protein
	(vi) ORIGINAL SOURCE:
45	(A) ORGANISM: <i>Serratia ficaria</i>
	(B) STRAIN: IAM 13540
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
	Met Lys Lys Ile Leu Leu Ala Thr Leu Ser Cys Ala Ala Leu Thr Gln

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      1           5           10           15
Phe Ser Phe Ala Ala Lys Asp Val Thr Thr His Pro Glu Val Tyr Phe
      20           25           30
5  Leu Gln Glu Ser Gln Ser Ile Asp Ser Leu Ala Leu Leu Pro Pro Pro
      35           40           45
Pro Ala Met Asp Ser Ile Asp Phe Leu Asn Asp Lys Ala Gln Tyr Asp
      50           55           60
Ala Gly Lys Ile Val Arg Asn Thr Pro Arg Gly Lys Gln Ala Tyr Asp
10  65           70           75           80
Asp Ala His Val Ala Gly Asp Gly Val Ala Ala Phe Ser Asn Ala
      85           90           95
Phe Gly Leu Glu Ile Ala Gln Arg Lys Thr Pro Glu Leu Phe Lys Leu
      100          105          110
15 Val Met Lys Met Arg Glu Asp Ala Gly Asp Leu Ala Thr Arg Ser Ala
      115          120          125
Lys Asn His Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Asn Glu Ala
      130          135          140
Thr Cys Arg Pro Asp Glu Glu Ser Thr Leu Ser Lys Asn Gly Ser Tyr
20  145          150          155          160
Pro Ser Gly His Thr Ile Gly Trp Ala Thr Ala Leu Val Leu Ala
      165          170          175
Glu Ile Asn Pro Ala Arg Gln Gly Glu Ile Leu Gln Arg Gly Tyr Asp
      180          185          190
25 Met Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser Asp Val
      195          200          205
Thr Ala Ala Arg Met Ala Ala Ser Ala Met Val Ala Arg Leu His Ala
      210          215          220
Glu Pro Thr Phe Ala Ala Gln Leu Gln Lys Ala Lys Asp Glu Phe Asn
30  225          230          235          240
Gly Leu Lys Lys

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INFORMATION FOR SEQ ID NO:29:

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      35  (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
      40  (ii) MOLECULE TYPE: other DNA..synthetic DNA
          (iii) HYPOTHETICAL: NO
          (iv) ANTI-SENSE: NO
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
          CCCGGCGTCA CCAATCATAT T

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21

45 INFORMATION FOR SEQ ID NO:30:

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      50  (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 21 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: other DNA..synthetic DNA
      55  (iii) HYPOTHETICAL: NO
          (iv) ANTI-SENSE: NO
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
          GCCGGTAGAG GCATGCCCGG A

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21

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

- 10 (A) NAME: Ajinomoto Co., Inc.
 (B) STREET: No.15-1, Kyobashi 1-chome, Chuo-ku
 (C) CITY: Tokyo
 (E) COUNTRY: Japan
 (F) POSTAL CODE (ZIP): 104 Japan

15 (ii) TITLE OF INVENTION: Method for producing nucleoside-5'-phosphate
 ester

20 (iii) NUMBER OF SEQUENCES: 30

(iv) COMPUTER READABLE FORM:

- 25 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

30 (v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 97309365.1

INFORMATION FOR SEQ ID NO:1:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide

(v) PROTEIN FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: Morganella morganii
 (B) STRAIN: NCIMB 10466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ile Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro Asp Leu Tyr Tyr
 1 5 10 15
 50 Leu Lys Asn Glu
 20

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INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Morganella morganii*

(B) STRAIN: NCIMB 10466

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..747

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..60

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 61..747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30	ATG AAG AAG AAT ATT ATC GCC GGT TGT CTG TTC TCA CTG TTT TCC CTT	48
	Met Lys Lys Asn Ile Ile Ala Gly Cys Leu Phe Ser Leu Phe Ser Leu	
	-20 -15 -10 -5	
	TCC GCG CTG GCC GCG ATC CCG GCG GGC AAC GAT GCC ACC ACC AAG CCG	96
35	Ser Ala Leu Ala Ala Ile Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro	
	1 5 10	
	GAT TTA TAT TAT CTG AAA AAT GAA CAG GCT ATC GAC AGC CTG AAA CTG	144
	Asp Leu Tyr Tyr Leu Lys Asn Glu Gln Ala Ile Asp Ser Leu Lys Leu	
40	15 20 25	
	TTA CCG CCA CCG CCG GAA GTC GGC AGT ATT CAG TTT TTA AAT GAT CAG	192
	Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Gln Phe Leu Asn Asp Gln	
	30 35 40	
45	GCA ATG TAT GAG AAA GGC CGT ATG CTG CGC AAT ACC GAG CGC GGA AAA	240
	Ala Met Tyr Glu Lys Gly Arg Met Leu Arg Asn Thr Glu Arg Gly Lys	
	45 50 55 60	
	CAG GCA CAG GCA GAT GCT GAC CTG GCC GCA GGG GGT GTG GCA ACC GCA	288
50	Gln Ala Gln Ala Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Thr Ala	
	65 70 75	
	TTT TCA GGG GCA TTC GGC TAT CCG ATA ACC GAA AAA GAC TCT CCG GAG	336
	Phe Ser Gly Ala Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ser Pro Glu	
55	80 85 90	

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CTG TAT AAA CTG CTG ACC AAT ATG ATT GAG GAT GCC GGT GAT CTT GCC 384
 Leu Tyr Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
 95 100 105
 5 ACC CGC TCC GCC AAA GAA CAT TAC ATG CGC ATC CGG CCG TTT GCG TTT 432
 Thr Arg Ser Ala Lys Glu His Tyr Met Arg Ile Arg Pro Phe Ala Phe
 110 115 120
 10 TAC GGC ACA GAA ACC TGT AAT ACC AAA GAT CAG AAA AAA CTC TCC ACC 480
 Tyr Gly Thr Glu Thr Cys Asn Thr Lys Asp Gln Lys Lys Leu Ser Thr
 125 130 135 140
 AAC GGA TCT TAC CCG TCA GGT CAT ACG TCT ATC GGC TGG GCA ACC GCA 528
 Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
 15 145 150 155
 CTG GTG CTG GCG GAA GTG AAC CCG GCA AAT CAG GAT GCG ATT CTG GAA 576
 Leu Val Leu Ala Glu Val Asn Pro Ala Asn Gln Asp Ala Ile Leu Glu
 160 165 170
 20 CGG GGT TAT CAG CTC GGA CAG AGC CGG GTG ATT TGC GGC TAT CAC TGG 624
 Arg Gly Tyr Gln Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
 175 180 185
 CAG AGT GAT GTG GAT GCC GCG CGG ATT GTC GGT TCA GCC GCT GTC GCG 672
 25 Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Ala Val Ala
 190 195 200
 ACA TTA CAT TCC GAT CCG GCA TTT CAG GCG CAG TTA GCG AAA GCC AAA 720
 Thr Leu His Ser Asp Pro Ala Phe Gln Ala Gln Leu Ala Lys Ala Lys
 30 205 210 215 220
 CAG GAA TTT GCA CAA AAA TCA CAG AAA TAA 750
 Gln Glu Phe Ala Gln Lys Ser Gln Lys
 225 229

35

INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Morganella morganii*
 (B) STRAIN: NCIMB 10466

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Lys Asn Ile Ile Ala Gly Cys Leu Phe Ser Leu Phe Ser Leu
 50 -20 -15 -10 -5
 Ser Ala Leu Ala Ala Ile Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro
 1 5 10
 55 Asp Leu Tyr Tyr Leu Lys Asn Glu Gln Ala Ile Asp Ser Leu Lys Leu
 15 20 25

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Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Gln Phe Leu Asn Asp Gln
 30 35 40
 Ala Met Tyr Glu Lys Gly Arg Met Leu Arg Asn Thr Glu Arg Gly Lys
 5 45 50 55 60
 Gln Ala Gln Ala Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Thr Ala
 65 70 75
 Phe Ser Gly Ala Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ser Pro Glu
 10 80 85 90
 Leu Tyr Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
 95 100 105
 Thr Arg Ser Ala Lys Glu His Tyr Met Arg Ile Arg Pro Phe Ala Phe
 15 110 115 120
 Tyr Gly Thr Glu Thr Cys Asn Thr Lys Asp Gln Lys Lys Leu Ser Thr
 125 130 135 140
 Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
 20 145 150 155
 Leu Val Leu Ala Glu Val Asn Pro Ala Asn Gln Asp Ala Ile Leu Glu
 160 165 170
 Arg Gly Tyr Gln Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
 25 175 180 185
 Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Ala Val Ala
 190 195 200
 Thr Leu His Ser Asp Pro Ala Phe Gln Ala Gln Leu Ala Lys Ala Lys
 30 205 210 215 220
 Gln Glu Phe Ala Gln Lys Ser Gln Lys
 225 229

INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Morganella morganii
 (B) STRAIN: NCIMB 10466
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 Ala Ile Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro Asp Leu Tyr Tyr
 1 5 10 15
 Leu Lys Asn Glu Gln Ala Ile Asp Ser Leu Lys Leu Leu Pro Pro Pro
 50 20 25 30
 Pro Glu Val Gly Ser Ile Gln Phe Leu Asn Asp Gln Ala Met Tyr Glu
 35 40 45
 Lys Gly Arg Met Leu Arg Asn Thr Glu Arg Gly Lys Gln Ala Gln Ala
 55 50 55 60

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Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Thr Ala Phe Ser Gly Ala
 65 70 75 80
 Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ser Pro Glu Leu Tyr Lys Leu
 5 85 90 95
 Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala Thr Arg Ser Ala
 100 105 110
 Lys Glu His Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Gly Thr Glu
 10 115 120 125
 Thr Cys Asn Thr Lys Asp Gln Lys Lys Leu Ser Thr Asn Gly Ser Tyr
 130 135 140
 Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala Leu Val Leu Ala
 15 145 150 155 160
 Glu Val Asn Pro Ala Asn Gln Asp Ala Ile Leu Glu Arg Gly Tyr Gln
 165 170 175
 Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser Asp Val
 20 180 185 190
 Asp Ala Ala Arg Ile Val Gly Ser Ala Ala Val Ala Thr Leu His Ser
 195 200 205
 Asp Pro Ala Phe Gln Ala Gln Leu Ala Lys Ala Lys Gln Glu Phe Ala
 25 210 215 220
 Gln Lys Ser Gln Lys
 225 229

30 INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - 35 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) PROTEIN FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - 40 (A) ORGANISM: Escherichia blattae
 - (B) STRAIN: JCM 1650
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Ala Leu Val Ala Thr Gly Asn Asp Thr Thr Lys Pro Asp Leu
 45 1 5 10 15

50 INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - 50 (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- 55 (iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia blattae*

(B) STRAIN: JCM 1650

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..747

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..54

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 55..747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20	ATG AAA AAA CGT GTT CTG GCA GTT TGT TTT GCC GCA TTG TTC TCT TCT	48
	Met Lys Lys Arg Val Leu Ala Val Cys Phe Ala Ala Leu Phe Ser Ser	
	-18 -15 -10 -5	
	CAG GCC CTG GCG CTG GTC GCT ACC GGC AAC GAC ACT ACC ACG AAA CCG	96
25	Gln Ala Leu Ala Leu Val Ala Thr Gly Asn Asp Thr Thr Thr Lys Pro	
	1 5 10	
	GAT CTC TAC TAC CTC AAG AAC AGT GAA GCC ATT AAC AGC CTG GCG CTG	144
	Asp Leu Tyr Tyr Leu Lys Asn Ser Glu Ala Ile Asn Ser Leu Ala Leu	
30	15 20 25 30	
	TTG CCG CCA CCA CCG GCG GTG GGC TCC ATT GCG TTT CTC AAC GAT CAG	192
	Leu Pro Pro Pro Pro Ala Val Gly Ser Ile Ala Phe Leu Asn Asp Gln	
	35 40 45	
35	GCC ATG TAT GAA CAG GGG CGC CTG CTG CGC AAC ACC GAA CGC GGT AAG	240
	Ala Met Tyr Glu Gln Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys	
	50 55 60	
	CTG GCG GCG GAA GAT GCA AAC CTG AGC AGT GGC GGG GTG GCG AAT GCT	288
40	Leu Ala Ala Glu Asp Ala Asn Leu Ser Ser Gly Gly Val Ala Asn Ala	
	65 70 75	
	TTC TCC GGC GCG TTT GGT AGC CCG ATC ACC GAA AAA GAC GCC CCG GCG	336
	Phe Ser Gly Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Ala	
45	80 85 90	
	CTG CAT AAA TTA CTG ACC AAT ATG ATT GAG GAC GCC GGG GAT CTG GCG	384
	Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala	
	95 100 105 110	
50	ACC CGC AGC GCG AAA GAT CAC TAT ATG CGC ATT CGT CCG TTC GCG TTT	432
	Thr Arg Ser Ala Lys Asp His Tyr Met Arg Ile Arg Pro Phe Ala Phe	
	115 120 125	
	TAT GGG GTC TCT ACC TGT AAT ACC ACC GAG CAG GAC AAA CTG TCC AAA	480
55	Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys	
	130 135 140	

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AAT GGC TCT TAT CCG TCC GGG CAT ACC TCT ATC GGC TGG GCT ACT GCG 528
 Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
 145 150 155
 5 CTG GTG CTG GCA GAG ATC AAC CCT CAG CGC CAG AAC GAG ATC CTG AAA 576
 Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
 160 165 170
 CGC GGT TAT GAG CTG GGC CAG AGC CGG GTG ATT TGC GGC TAC CAC TGG 624
 10 Arg Gly Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
 175 180 185 190
 CAG AGT GAT GTG GAT GCC GCG CGG GTA GTG GGA TCT GCC GTT GTG GCG 672
 Gln Ser Asp Val Asp Ala Ala Arg Val Val Gly Ser Ala Val Val Ala
 195 200 205
 15 ACC CTG CAT ACC AAC CCG GCG TTC CAG CAG CAG TTG CAG AAA GCG AAG 720
 Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
 210 215 220
 20 GCC GAA TTC GCC CAG CAT CAG AAG AAA TAA 750
 Ala Glu Phe Ala Gln His Gln Lys Lys
 225 230

INFORMATION FOR SEQ ID NO:7:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Escherichia blattae
 (B) STRAIN: JCM 1650
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
 Met Lys Lys Arg Val Leu Ala Val Cys Phe Ala Ala Leu Phe Ser Ser
 -18 -15 -10 -5
 Gln Ala Leu Ala Leu Val Ala Thr Gly Asn Asp Thr Thr Thr Lys Pro
 40 1 5 10
 Asp Leu Tyr Tyr Leu Lys Asn Ser Glu Ala Ile Asn Ser Leu Ala Leu
 15 20 25 30
 Leu Pro Pro Pro Pro Ala Val Gly Ser Ile Ala Phe Leu Asn Asp Gln
 45 35 40 45
 Ala Met Tyr Glu Gln Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys
 50 55 60
 Leu Ala Ala Glu Asp Ala Asn Leu Ser Ser Gly Gly Val Ala Asn Ala
 65 70 75
 50 Phe Ser Gly Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Ala
 80 85 90
 Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
 95 100 105 110
 55

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Thr Arg Ser Ala Lys Asp His Tyr Met Arg Ile Arg Pro Phe Ala Phe
 115 120 125
 Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys
 5 130 135 140
 Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
 145 150 155
 Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
 10 160 165 170
 Arg Gly Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
 175 180 185 190
 Gln Ser Asp Val Asp Ala Ala Arg Val Val Gly Ser Ala Val Val Ala
 15 195 200 205
 Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
 210 215 220
 Ala Glu Phe Ala Gln His Gln Lys Lys
 20 225 230

INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Escherichia blattae
 (B) STRAIN: JCM 1650
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
 35 Leu Ala Leu Val Ala Thr Gly Asn Asp Thr Thr Lys Pro Asp Leu
 1 5 10 15
 Tyr Tyr Leu Lys Asn Ser Glu Ala Ile Asn Ser Leu Ala Leu Leu Pro
 20 25 30
 Pro Pro Pro Ala Val Gly Ser Ile Ala Phe Leu Asn Asp Gln Ala Met
 40 35 40 45
 Tyr Glu Gln Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys Leu Ala
 50 55 60
 Ala Glu Asp Ala Asn Leu Ser Ser Gly Gly Val Ala Asn Ala Phe Ser
 45 65 70 75 80
 Gly Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Ala Leu His
 85 90 95
 Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala Thr Arg
 50 100 105 110
 Ser Ala Lys Asp His Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Gly
 115 120 125
 Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys Asn Gly
 55 130 135 140

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Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala Leu Val
 145 150 155 160
 5 Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys Arg Gly
 165 170 175
 Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser
 180 185 190
 10 Asp Val Asp Ala Ala Arg Val Val Gly Ser Ala Val Val Ala Thr Leu
 195 200 205
 His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys Ala Glu
 210 215 220
 Phe Ala Gln His Gln Lys Lys
 15 225 230

INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 30 CCTCGAGGTC GACGGTATCG 20

INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: YES
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
 45 ATTCGCCACA TCGCCACTGC T 21

INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
 5 TAGCCCAGCC GGTAGAGGTA TG 22

INFORMATION FOR SEQ ID NO:12:
 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
 TGCATCTGCC TCGCCTGCT TAC 23

INFORMATION FOR SEQ ID NO:13:
 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
 AACGCGCCGT AGAAAGCATT 20

INFORMATION FOR SEQ ID NO:14:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other DNA..synthetic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
 GTCCTGGTCT TTGGTATTAC A 21

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INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA..synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CACATCGCCA GCGCCAGGT CTGCAT

26

INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA..synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCATATAGTG TTCTTCGCG C

21

INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA..synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATTACAGGTT TCGACCCCAT AA

22

INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA..synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
TGATGCATGT CCGGGCTGTC TTTT

25

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INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA..synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
CTGGATCCTG TGGCTATCAT CACCT

25

20

INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other DNA..synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
CTGGATCCGA CGCGATTTTA CCATA

25

35

INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Providencia stuartii

(B) STRAIN: ATCC 29851

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..744

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

	ATG AAA AAA CTA TTA GCA GTA TTC TGC GCA GGG GCT TTT GTT TCA ACC	48
5	Met Lys Lys Leu Leu Ala Val Phe Cys Ala Gly Ala Phe Val Ser Thr	
	1 5 10 15	
	AGT GTA TTT GCG GCG ATC CCT CCC GGC AAT GAT GTG ACA ACT AAA CCC	96
	Ser Val Phe Ala Ala Ile Pro Pro Gly Asn Asp Val Thr Thr Lys Pro	
10	20 25 30	
	GAT CTT TAT TAT TTA AAA AAC TCA CAG GCT ATT GAT AGT TTA GCG TTA	144
	Asp Leu Tyr Tyr Leu Lys Asn Ser Gln Ala Ile Asp Ser Leu Ala Leu	
	35 40 45	
15	TTG CCG CCA CCA CCT GAA GTG GGC AGT ATC TTA TTT TTA AAC GAC CAA	192
	Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Leu Phe Leu Asn Asp Gln	
	50 55 60	
	GCG ATG TAT GAA AAA GGC CGT TTA TTG CGA AAT ACT GAG CGT GGA GAA	240
20	Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Glu	
	65 70 75 80	
	CAA GCC GCT AAG GAT GCT GAT CTG GCT GCG GGC GGT GTT GCG AAC GCA	288
	Gln Ala Ala Lys Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Asn Ala	
25	85 90 95	
	TTT TCT GAA GCT TTT GGT TAT CCC ATT ACC GAA AAG GAT GCG CCT GAA	336
	Phe Ser Glu Ala Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ala Pro Glu	
	100 105 110	
30	ATT CAT AAA TTG CTG ACG AAT ATG ATT GAA GAT GCG GGC GAT TTA GCA	384
	Ile His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala	
	115 120 125	
	ACT CGC TCA GCC AAA GAG AAA TAC ATG CGC ATT CGT CCA TTT GCG TTC	432
35	Thr Arg Ser Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe	
	130 135 140	
	TAC GGT GTT GCT ACC TGT AAC ACG AAA GAT CAG GAC AAA TTA TCT AAG	480
	Tyr Gly Val Ala Thr Cys Asn Thr Lys Asp Gln Asp Lys Leu Ser Lys	
40	145 150 155 160	
	AAT GGC TCT TAT CCT TCT GGA CAC ACC GCA ATT GGC TGG GCA TCT GCA	528
	Asn Gly Ser Tyr Pro Ser Gly His Thr Ala Ile Gly Trp Ala Ser Ala	
	165 170 175	
45	CTC GTA TTG TCA GAA ATT AAC CCA GAA AAC CAA GAT AAA ATT TTA AAA	576
	Leu Val Leu Ser Glu Ile Asn Pro Glu Asn Gln Asp Lys Ile Leu Lys	
	180 185 190	
	CGT GGT TAT GAA CTT GGC CAA AGC CGA GTC ATC TGT GGT TAC CAT TGG	624
50	Arg Gly Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp	
	195 200 205	
	CAA AGT GAT GTT GAT GCA GCT CGT ATC GTT GCA TCG GGT GCG GTA GCA	672
	Gln Ser Asp Val Asp Ala Ala Arg Ile Val Ala Ser Gly Ala Val Ala	
55	210 215 220	

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ACT TTA CAC TCC AAC CCT GAA TTC CAA AAA CAG TTA CAA AAA GCC AAA 720
 Thr Leu His Ser Asn Pro Glu Phe Gln Lys Gln Leu Gln Lys Ala Lys
 225 230 235 240
 5 GAC GAA TTT GCT AAA CTG AAA AAA TAG 747
 Asp Glu Phe Ala Lys Leu Lys Lys
 245

10

INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 15 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Providencia stuartii
 20 (B) STRAIN: ATCC 29851
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 Met Lys Lys Leu Leu Ala Val Phe Cys Ala Gly Ala Phe Val Ser Thr
 1 5 10 15
 25 Ser Val Phe Ala Ala Ile Pro Pro Gly Asn Asp Val Thr Thr Lys Pro
 20 25 30
 Asp Leu Tyr Tyr Leu Lys Asn Ser Gln Ala Ile Asp Ser Leu Ala Leu
 35 40 45
 30 Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Leu Phe Leu Asn Asp Gln
 50 55 60
 Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Glu
 65 70 75 80
 35 Gln Ala Ala Lys Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Asn Ala
 85 90 95
 Phe Ser Glu Ala Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ala Pro Glu
 100 105 110
 40 Ile His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
 115 120 125
 Thr Arg Ser Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe
 130 135 140
 45 Tyr Gly Val Ala Thr Cys Asn Thr Lys Asp Gln Asp Lys Leu Ser Lys
 145 150 155 160
 Asn Gly Ser Tyr Pro Ser Gly His Thr Ala Ile Gly Trp Ala Ser Ala
 165 170 175
 50 Leu Val Leu Ser Glu Ile Asn Pro Glu Asn Gln Asp Lys Ile Leu Lys
 180 185 190
 Arg Gly Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
 195 200 205
 55 Gln Ser Asp Val Asp Ala Ala Arg Ile Val Ala Ser Gly Ala Val Ala
 210 215 220

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Thr Leu His Ser Asn Pro Glu Phe Gln Lys Gln Leu Gln Lys Ala Lys
 225 230 235 240
 Asp Glu Phe Ala Lys Leu Lys Lys
 245

INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 744 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Enterobacter aerogenes

(B) STRAIN: IFO 12010

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG AAA AAG CGC GTT CTC GCC CTC TGC CTC GCC AGC CTG TTT TCC GTT	48
Met Lys Lys Arg Val Leu Ala Leu Cys Leu Ala Ser Leu Phe Ser Val	
1 5 10 15	
AAC GCT TTC GCG CTG GTC CCT GCC GGC AAT GAT GCA ACC ACC AAA CCG	96
Asn Ala Phe Ala Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro	
20 25 30	
GAT CTC TAT TAT CTG AAA AAT GCA CAG GCC ATC GAT AGT CTG GCG CTG	144
Asp Leu Tyr Tyr Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu	
35 40 45	
TTG CCG CCG CCG CCG GAA GTT GGC AGC ATC GCA TTT TTA AAC GAT CAG	192
Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln	
50 55 60	
GCG ATG TAT GAG AAA GGA CGG CTG TTG CGC AAT ACC GAA CGT GGC AAG	240
Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys	
65 70 75 80	
CTG GCG GCT GAA GAT GCT AAC CTG AGC GCC GGC GGC GTC GCG AAT GCC	288
Leu Ala Ala Glu Asp Ala Asn Leu Ser Ala Gly Gly Val Ala Asn Ala	
85 90 95	
TTC TCC AGC GCT TTT GGT TCG CCC ATC ACC GAA AAA GAC GCG CCG CAG	336
Phe Ser Ser Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Gln	
100 105 110	
TTA CAT AAG CTG CTG ACA AAT ATG ATT GAG GAT GCC GGC GAT CTG GCC	384
Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala	
115 120 125	

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ACC CGC AGC GCG AAA GAG AAA TAT ATG CGC ATT CGC CCG TTT GCG TTC 432
 Thr Arg Ser Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe
 130 135 140
 5 TAC GGC GTT TCA ACC TGT AAC ACT ACC GAG CAG GAC AAG CTG TCG AAA 480
 Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys
 145 150 155 160
 10 AAC GGA TCT TAC CCT TCC GGC CAT ACC TCT ATC GGT TGG GCA ACC GCG 528
 Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
 165 170 175
 CTG GTA CTG GCG GAG ATC AAT CCG CAG CGG CAA AAC GAA ATT CTC AAA 576
 Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
 15 180 185 190
 CGC GGC TAT GAA TTG GGC GAA AGC CGG GTT ATC TGC GGC TAT CAT TGG 624
 Arg Gly Tyr Glu Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp
 195 200 205
 20 CAG AGC GAT GTC GAT GCG GCG CGG ATA GTC GGC TCG GCG GTG GTG GCG 672
 Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala
 210 215 220
 ACC CTG CAT ACC AAC CCG GCC TTC CAA CAG CAG TTG CAG AAA GCA AAG 720
 25 Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
 225 230 235 240
 GAT GAA TTC GCC AAA ACG CAG AAG TAA 747
 Asp Glu Phe Ala Lys Thr Gln Lys
 30 245

INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Enterobacter aerogenes
 (B) STRAIN: IFO 12010
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
 45 Met Lys Lys Arg Val Leu Ala Leu Cys Leu Ala Ser Leu Phe Ser Val
 1 5 10 15
 Asn Ala Phe Ala Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro
 20 25 30
 50 Asp Leu Tyr Tyr Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu
 35 40 45
 Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln
 50 55 60
 55 Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys
 65 70 75 80

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Leu Ala Ala Glu Asp Ala Asn Leu Ser Ala Gly Gly Val Ala Asn Ala
85 90 95
Phe Ser Ser Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Gln
5 100 105 110
Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
115 120 125
Thr Arg Ser Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe
10 130 135 140
Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys
145 150 155 160
Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
15 165 170 175
Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
180 185 190
Arg Gly Tyr Glu Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp
20 195 200 205
Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala
210 215 220
Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
225 230 235 240
25 Asp Glu Phe Ala Lys Thr Gln Lys
245

30 INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(iii) HYPOTHETICAL: NO
40 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Klebsiella planticola
(B) STRAIN: IFO 14939
45 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..747
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
50 ATG AAA AAG CGT GTA CTC GCC CTT TGC CTT GCC AGC CTC TTT TCA GTT 48
Met Lys Lys Arg Val Leu Ala Leu Cys Leu Ala Ser Leu Phe Ser Val
1 5 10 15

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	AGC GCC TTT GCG CTG GTT CCC GCC GGC AAT GAT GCC ACC ACC AAG CCC	96
	Ser Ala Phe Ala Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro	
	20 25 30	
5	GAT CTC TAC TAT CTG AAA AAT GCC CAG GCC ATT GAC AGC CTG GCG CTG	144
	Asp Leu Tyr Tyr Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu	
	35 40 45	
10	TTG CCA CCG CCG CCG GAA GTG GGC AGC ATT GCG TTT TTA AAC GAT CAG	192
	Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln	
	50 55 60	
	GCG ATG TAT GAG AAA GGC CGT CTG CTG CGC GCC ACC GCC CGC GGC AAG	240
	Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Ala Thr Ala Arg Gly Lys	
15	65 70 75 80	
	TTG GCG GCA GAA GAT GCC AAC CTG AGC GCG GGT GGC GTG GCC AAC GCC	288
	Leu Ala Ala Glu Asp Ala Asn Leu Ser Ala Gly Gly Val Ala Asn Ala	
	85 90 95	
20	TTC TCC GCA GCA TTC GGC TCC CCG ATC AGC GAA AAA GAC GCC CCG GCG	336
	Phe Ser Ala Ala Phe Gly Ser Pro Ile Ser Glu Lys Asp Ala Pro Ala	
	100 105 110	
25	CTG CAC AAA CTG CTC ACC AAC ATG ATT GAA GAC GCG GGC GAT CTG GCG	384
	Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala	
	115 120 125	
	ACC CGA GGC GCG AAA GAG AAG TAT ATG CGT ATT CGT CCG TTT GCC TTC	432
	Thr Arg Gly Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe	
30	130 135 140	
	TAC GGC GTG TCC ACC TGC AAT ACC ACC GAA CAG GAT AAG CTG TCG AAA	480
	Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys	
	145 150 155 160	
35	AAC GGC TCC TAC CCT TCC GGA CAC ACC TCT ATC GGC TGG GCG ACC GCC	528
	Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala	
	165 170 175	
40	CTG GTG CTG GCC GAA ATC AAC CCG CAG CGC CAG AAT GAG ATT CTC AAG	576
	Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys	
	180 185 190	
	CGC GGC TAT GAG CTC GGT GAA AGT CGG GTG ATC TGC GGT TAC CAC TGG	624
	Arg Gly Tyr Glu Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp	
45	195 200 205	
	CAG AGC GAT GTT GAC GCC GCG CGG ATT GTC GGC TCG GCG GTG GTT GCA	672
	Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala	
	210 215 220	
50	ACC CTG CAT ACC AAT CCG GCC TTC CAG CAG CAG CTG CAA AAA GCC AAA	720
	Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys	
	225 230 235 240	
	GAC GAG TTT GCG AAA CAG CAG AAA TAG	747
55	Asp Glu Phe Ala Lys Gln Gln Lys	
	245	

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INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: IFO 14939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Lys Lys Arg Val Leu Ala Leu Cys Leu Ala Ser Leu Phe Ser Val
1 5 10 15
Ser Ala Phe Ala Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro
20 25 30
Asp Leu Tyr Tyr Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu
35 40 45
Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln
50 55 60
Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Ala Thr Ala Arg Gly Lys
65 70 75 80
Leu Ala Ala Glu Asp Ala Asn Leu Ser Ala Gly Gly Val Ala Asn Ala
85 90 95
Phe Ser Ala Ala Phe Gly Ser Pro Ile Ser Glu Lys Asp Ala Pro Ala
100 105 110
Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
115 120 125
Thr Arg Gly Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe
130 135 140
Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys
145 150 155 160
Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
165 170 175
Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
180 185 190
Arg Gly Tyr Glu Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp
195 200 205
Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala
210 215 220
Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
225 230 235 240
Asp Glu Phe Ala Lys Gln Gln Lys
245

INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia ficaria*

(B) STRAIN: IAM 13540

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

5	ATG AAA AAA ATA TTA TTA GCC ACA TTA AGC TGC GCC GCG TTG ACG CAG	48
	Met Lys Lys Ile Leu Leu Ala Thr Leu Ser Cys Ala Ala Leu Thr Gln	
	1 5 10 15	
25	TTT TCC TTT GCC GCC AAA GAT GTC ACT ACC CAC CCT GAG GTT TAT TTT	96
	Phe Ser Phe Ala Ala Lys Asp Val Thr Thr His Pro Glu Val Tyr Phe	
	20 25 30	
30	CTG CAA GAA TCA CAG TCC ATC GAC AGC CTG GCA CTA TTG CCG CCG CCG	144
	Leu Gln Glu Ser Gln Ser Ile Asp Ser Leu Ala Leu Leu Pro Pro Pro	
	35 40 45	
35	CCG GCG ATG GAC AGC ATT GAT TTC CTG AAT GAC AAA GCG CAA TAC GAC	192
	Pro Ala Met Asp Ser Ile Asp Phe Leu Asn Asp Lys Ala Gln Tyr Asp	
	50 55 60	
	GCC GGG AAA ATA GTG CGC AAT ACT CCG CGT GGC AAG CAG GCT TAT GAT	240
	Ala Gly Lys Ile Val Arg Asn Thr Pro Arg Gly Lys Gln Ala Tyr Asp	
	65 70 75 80	
40	GAC GCC CAC GTT GCC GGG GAC GGC GTT GCC GCC GCA TTT TCC AAC GCC	288
	Asp Ala His Val Ala Gly Asp Gly Val Ala Ala Ala Phe Ser Asn Ala	
	85 90 95	
45	TTC GGC CTA GAA ATA GCC CAA CGG AAA ACG CCG GAG CTG TTT AAG CTG	336
	Phe Gly Leu Glu Ile Ala Gln Arg Lys Thr Pro Glu Leu Phe Lys Leu	
	100 105 110	
	GTG ATG AAA ATG CGT GAA GAC GCC GGC GAT TTG GCG ACC CGC AGC GCC	384
	Val Met Lys Met Arg Glu Asp Ala Gly Asp Leu Ala Thr Arg Ser Ala	
	115 120 125	
50	AAA AAT CAC TAT ATG CGC ATT CGC CCC TTT GCG TTT TAT AAC GAA GCG	432
	Lys Asn His Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Asn Glu Ala	
	130 135 140	
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ACC TGC CGA CCG GAC GAA GAA AGC ACC CTG TCG AAG AAC GGT TCT TAC 480
 Thr Cys Arg Pro Asp Glu Glu Ser Thr Leu Ser Lys Asn Gly Ser Tyr
 145 150 155 160
 5 CCT TCC GGC CAT ACC ACC ATC GGC TGG GCG ACC GCG CTG GTG CTG GCT 528
 Pro Ser Gly His Thr Thr Ile Gly Trp Ala Thr Ala Leu Val Leu Ala
 165 170 175
 GAA ATC AAC CCC GCC AGG CAG GGT GAA ATC CTG CAG CGC GGC TAT GAT 576
 10 Glu Ile Asn Pro Ala Arg Gln Gly Glu Ile Leu Gln Arg Gly Tyr Asp
 180 185 190
 ATG GGC CAA AGC CGG GTT ATC TGC GGT TAT CAC TGG CAA AGC GAC GTG 624
 Met Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser Asp Val
 15 195 200 205
 ACT GCG GCG CGC ATG GCG GCG TCG GCC ATG GTG GCG CGT TTG CAT GCC 672
 Thr Ala Ala Arg Met Ala Ala Ser Ala Met Val Ala Arg Leu His Ala
 210 215 220
 20 GAA CCC ACC TTC GCC GCC CAG CTG CAA AAG GCC AAA GAC GAA TTC AAC 720
 Glu Pro Thr Phe Ala Ala Gln Leu Gln Lys Ala Lys Asp Glu Phe Asn
 225 230 235 240
 GGC CTG AAA AAG TAA 735
 25 Gly Leu Lys Lys

INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 244 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia ficaria*
 (B) STRAIN: IAM 13540
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
 40 Met Lys Lys Ile Leu Leu Ala Thr Leu Ser Cys Ala Ala Leu Thr Gln
 1 5 10 15
 Phe Ser Phe Ala Ala Lys Asp Val Thr Thr His Pro Glu Val Tyr Phe
 20 25 30
 45 Leu Gln Glu Ser Gln Ser Ile Asp Ser Leu Ala Leu Leu Pro Pro Pro
 35 40 45
 Pro Ala Met Asp Ser Ile Asp Phe Leu Asn Asp Lys Ala Gln Tyr Asp
 50 55 60
 50 Ala Gly Lys Ile Val Arg Asn Thr Pro Arg Gly Lys Gln Ala Tyr Asp
 65 70 75 80
 Asp Ala His Val Ala Gly Asp Gly Val Ala Ala Ala Phe Ser Asn Ala
 85 90 95
 55 Phe Gly Leu Glu Ile Ala Gln Arg Lys Thr Pro Glu Leu Phe Lys Leu
 100 105 110

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Val Met Lys Met Arg Glu Asp Ala Gly Asp Leu Ala Thr Arg Ser Ala
 115 120 125
 5 Lys Asn His Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Asn Glu Ala
 130 135 140
 Thr Cys Arg Pro Asp Glu Glu Ser Thr Leu Ser Lys Asn Gly Ser Tyr
 145 150 155 160
 10 Pro Ser Gly His Thr Thr Ile Gly Trp Ala Thr Ala Leu Val Leu Ala
 165 170 175
 Glu Ile Asn Pro Ala Arg Gln Gly Glu Ile Leu Gln Arg Gly Tyr Asp
 180 185 190
 15 Met Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser Asp Val
 195 200 205
 Thr Ala Ala Arg Met Ala Ala Ser Ala Met Val Ala Arg Leu His Ala
 210 215 220
 20 Glu Pro Thr Phe Ala Ala Gln Leu Gln Lys Ala Lys Asp Glu Phe Asn
 225 230 235 240
 Gly Leu Lys Lys

25 INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - 30 (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other DNA..synthetic DNA
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCGGCGTCA CCAATCATAT T

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40 INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - 45 (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other DNA..synthetic DNA
- (iii) HYPOTHETICAL: NO
- 50 (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCGGTAGAG GCATGCCCGG A

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Claims

1. A method for producing nucleoside-5'-phosphate ester comprising the steps of allowing an acid phosphatase having an increased affinity for the nucleoside and/or an increased temperature stability to act under a condition of pH 3.0 to 5.5 on a nucleoside and a phosphate group donor to produce nucleoside-5'-phosphate ester, and collecting it.
2. A method for producing nucleoside-5'-phosphate ester comprising the steps of allowing a microorganism to act under a condition of pH 3.0 to 5.5 on a nucleoside and a phosphate group donor to produce nucleoside-5'-phosphate ester, and collecting it, wherein the microorganism is transformed with a recombinant DNA comprising a gene encoding an acid phosphatase having an increased affinity for the nucleoside and/or an increased temperature stability.
3. The method for producing nucleoside-5'-phosphate ester according to claims 1 or 2, wherein the K_m value for the nucleoside is below 100.
4. The method for producing nucleoside-5'-phosphate ester according to claims 1 or 2, wherein the acid phosphatase is stable at 50°C.
5. The method for producing nucleoside-5'-phosphate ester according to claims 1 or 2, wherein the acid phosphatase having an increased affinity for the nucleoside is derived from a bacterium belonging to the genus Escherichia, the genus Morganella, the genus Providencia, the genus Enterobacter, the genus Klebsiella or the genus Serratia.
6. The method for producing nucleoside-5'-phosphate ester according to claim 5, wherein the acid phosphatase comprises an amino acid sequence which is substantially identical with an amino acid sequence selected from the group consisting of sequences illustrated in SEQ ID NOs: 4, 8, 25, 27, 29 and 31 in Sequence Listing, and said acid phosphatase has a mutation which increases the affinity for the nucleoside and/or the temperature stability on an amino acid sequence selected from the group consisting of sequences illustrated in SEQ ID NOs: 4, 8, 25, 27, 29 and 31 in Sequence Listing.
7. The method for producing nucleoside-5'-phosphate ester according to claim 5, wherein said mutation is selected from the group consisting of substitutions of the 63rd leucine residue, the 65th alanine residue, the 66th glutamic acid residue, the 69th aspartic acid residue, the 71st serine residue, the 72nd serine residue, the 74th glycine residue, the 85th serine residue, the 92nd alanine residue, the 94th alanine residue, the 104th glutamic acid residue, the 116th aspartic acid residue, the 130th serine residue, the 135th threonine residue, the 136th glutamic acid residue, the 151th threonine residue and/or the 153rd isoleucine residue with another amino acid in SEQ ID NO: 8 in Sequence Listing.
8. The method for producing nucleoside-5'-phosphate ester according to claims 1 or 2, wherein said phosphate group donor is selected from the group consisting of polyphosphoric acid or a salt thereof, phenylphosphoric acid or a salt thereof, acetylphosphoric acid or a salt thereof, and carbamyl phosphate or a salt thereof.
9. A mutant acid phosphatase comprising an amino acid sequence which is substantially identical with an amino acid sequence selected from the group consisting of sequences illustrated in SEQ ID NOs: 4, 8, 25, 27, 29 and 31 in Sequence Listing, and said acid phosphatase has a mutation which increases the affinity for the nucleoside and/or the temperature stability on an amino acid sequence selected from the group consisting of sequences illustrated in SEQ ID NOs: 4, 8, 25, 27, 29 and 31 in Sequence Listing.
10. A mutant acid phosphatase according to claim 9, wherein said mutation is selected from the group consisting of substitutions of the 63rd leucine residue, the 65th alanine residue, the 66th glutamic acid residue, the 69th aspartic acid residue, the 71st serine residue, the 72nd serine residue, the 74th glycine residue, the 85th serine residue, the 92nd alanine residue, the 94th alanine residue, the 104th threonine residue, the 116th aspartic acid residue, the 130th serine residue, the 135th threonine residue, the 136th glutamic acid residue, the 151st threonine residue and/or the 153rd isoleucine residue with another amino acid in SEQ ID NO: 8 in Sequence Listing.
11. A gene coding for the acid phosphatase as defined in claim 9
12. A recombinant DNA comprising the gene as defined in claim 11.

13. A microorganism harboring the recombinant DNA as defined in claim 12.

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Fig 1

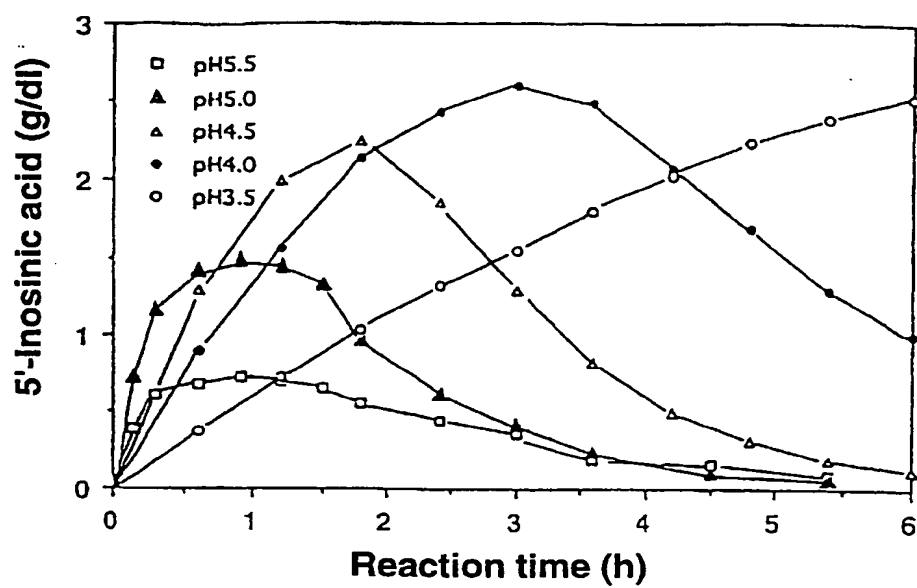


Fig 2

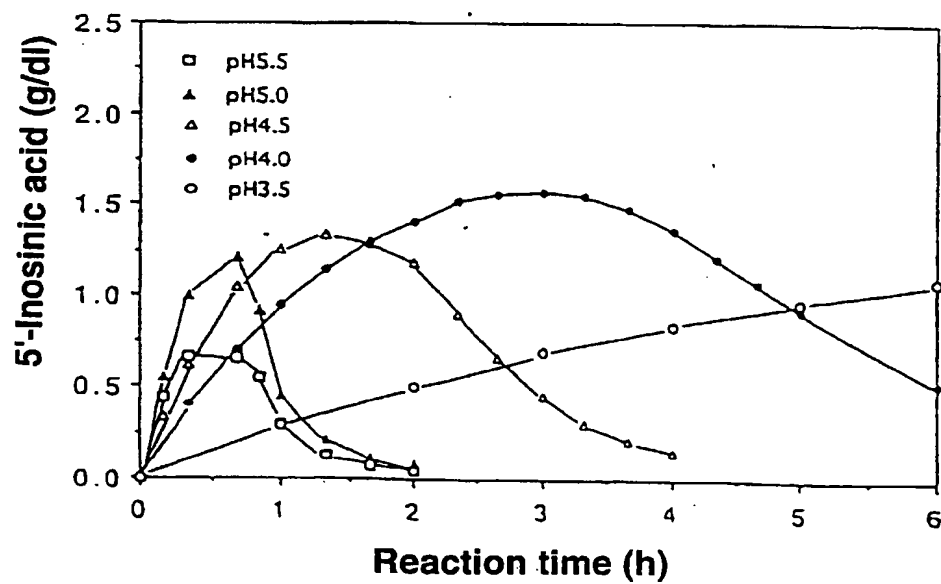
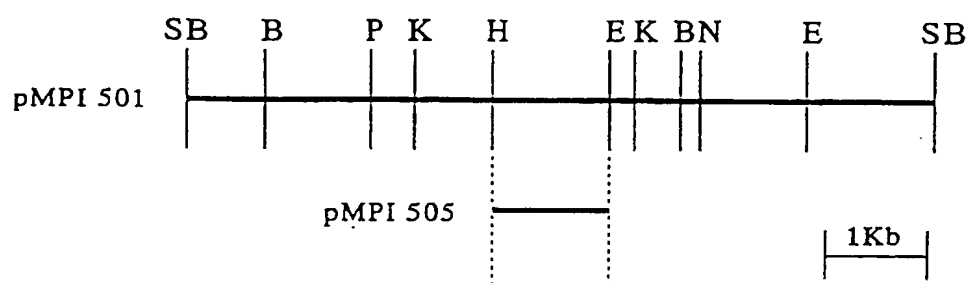
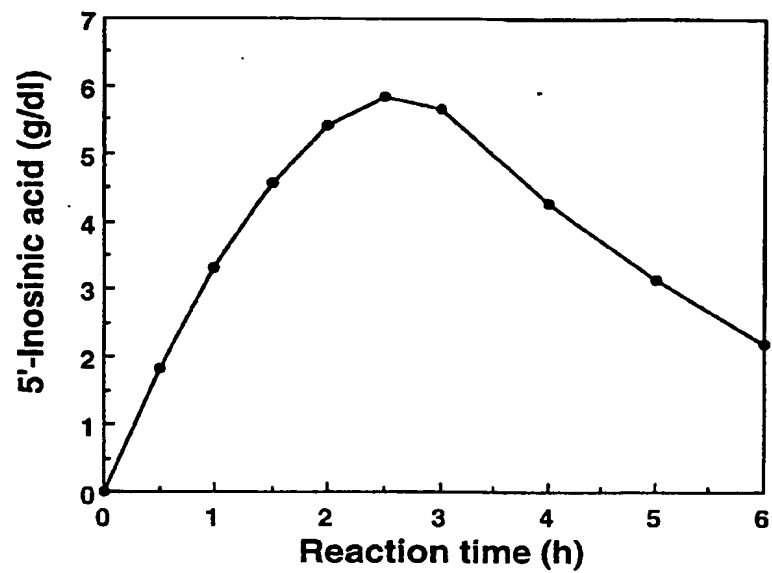


FIG. 3



SB: *Sau3AI* / *Bam*HI junction B: *Bam* HI E: *Eco*RI K: *Kpn*I
H: *Hind*III N: *Nco*I P: *Pst*I

【Fig.4】



【Fig.6】

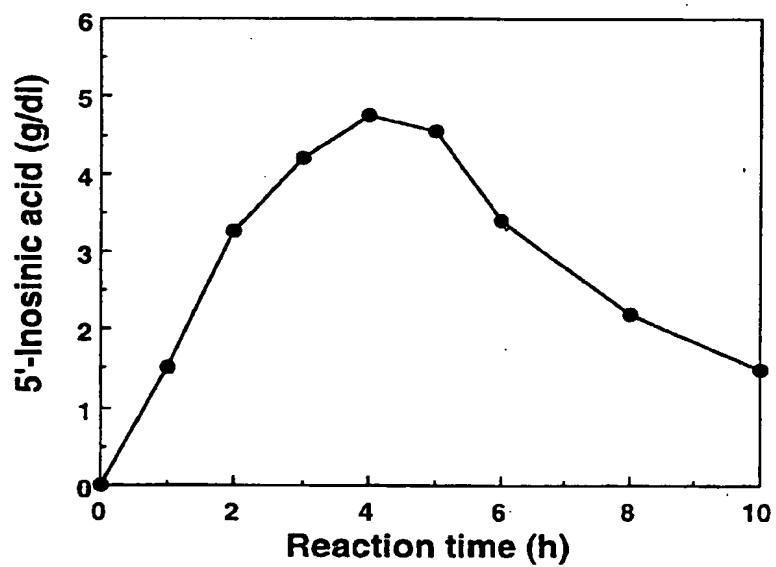
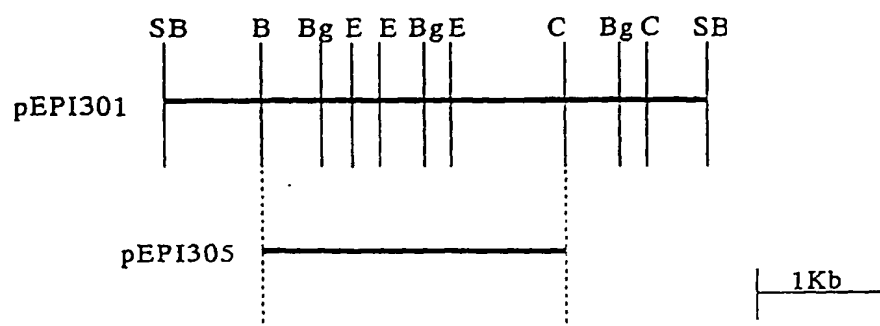


FIG. 5



SB: *Sau*3AI / *Bam*HI junction B: *Bam*HI Bg: *Bgl*II C: *Cla*I E: *Eco*RI

[Fig.7]

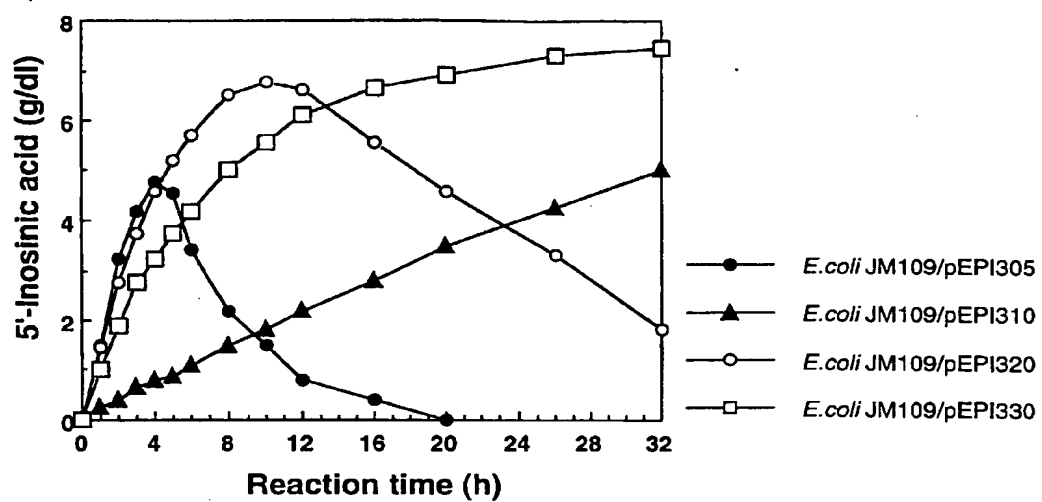


Fig 8

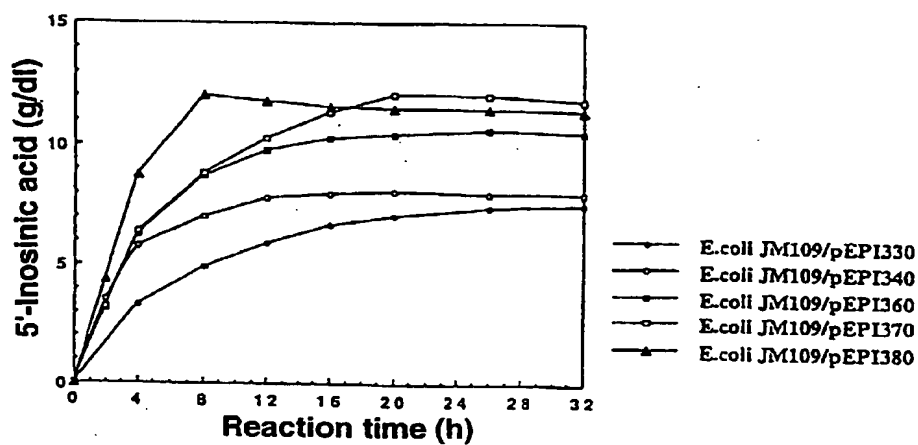


Fig 13

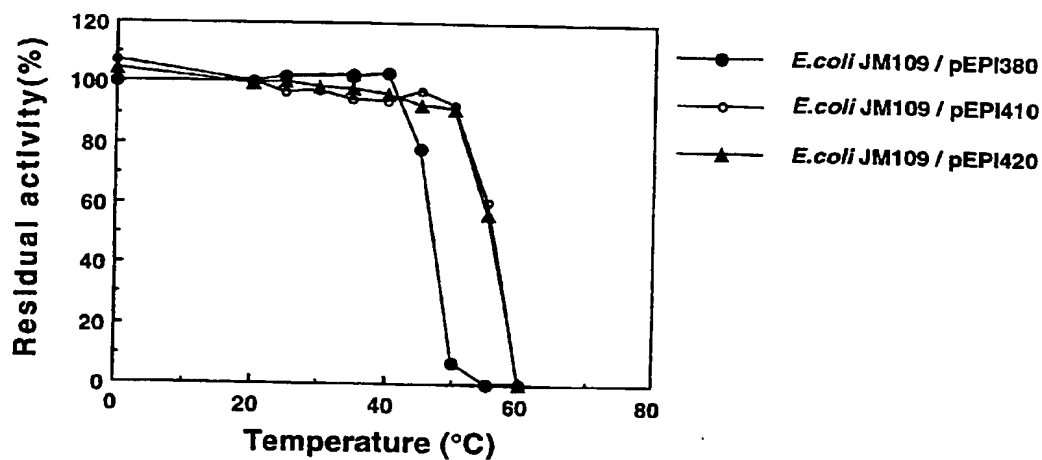
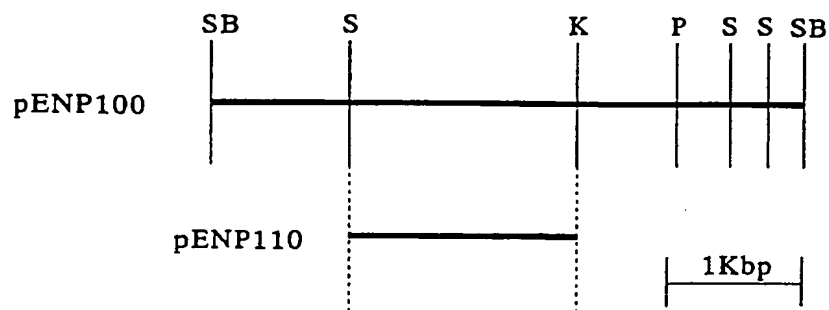
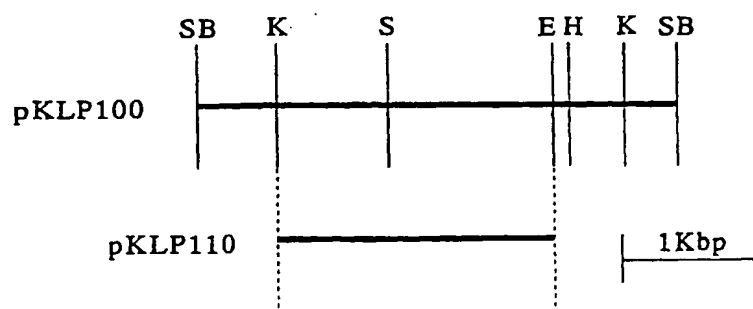


FIG. 9



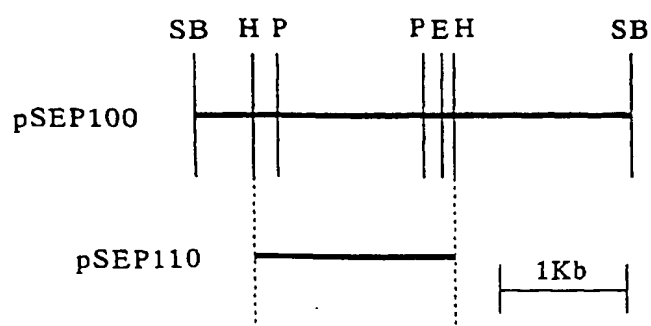
SB: *Sau*3AI / *Bam*HI junction K: *Kpn*I P: *Pst*I S: *Sal*I

FIG. 10



SB: *Sau*3AI / *Bam*HI junction E: *Eco*RI H: *Hind*III K: *Kpn*I
S: *Sac*I

F I G. 1 1



SB: *Sau3AI* / *Bam*HI junction E: *EcoRI* H: *Hind*III P: *Pst*I

FIG. 12

E. aerogenes	1:MKKRYLALCLASLFSVNAFALVPAGNDATTKPDLYYLKNAQAIDSLALLP	50
E. blattae	1:MKKRYLAVCFALFSSQALALVATGNDTTTKPDLYYLKNSEAINSLALLP	50
K. planticola	1:MKKRYLALCLASLFSVSFAFALVPAGNDATTKPDLYYLKNAQAIDSLALLP	50
M. morgani	1:MKKNIIAGCLFSLFSLALAAIPAGNDATTKPDLYYLKNEQAIDSLKLLP	50
P. stuartii	1:MKKLLAVFCAGAFYSTSVFAAIPPGNDVTTKPDLYYLKNSQAIDSLALLP	50
S. ficaria	1:MKK-ILLA-TLSCAALTQFS--FAAKDYTTTPEVYFLQESQSIDSLALLP	46
	*** * * * * *	
E. aerogenes	51:PPPEVGSIAFLNDQAMYEGRLLRNTERGKLAEDANLSAGGVANAFSSA	100
E. blattae	51:PPPAVGSI AFLNDQAMYEQGRLLRNTERGKLAEDANLSSGGVANAFSGA	100
K. planticola	51:PPPEVGSIAFLNDQAMYEGRLLRATARGKLAEDANLSAGGVANAFSAA	100
M. morgani	51:PPPEVGSIAFLNDQAMYEGRMLRNTERGKQAQADADLAAGGVATAFSGA	100
P. stuartii	51:PPPEVGSILFLNDQAMYEGRLLRNTERGEQAADADLAAGGVANAFSEA	100
S. ficaria	47:PPPAMDSIDFLNDKAQYDAGKIVRNTPRGKQAYDDAHVAGDGVAAAFSNA	96
	*** * * * * *	
E. aerogenes	101:FGSPITEKDAPQLHKLLTNMIEDAGDLATRSACEKYMRI RPF AFYGVSTC	150
E. blattae	101:FGSPITEKDAPALHKLLTNMIEDAGDLATRSADHYMRI RPF AFYGVSTC	150
K. planticola	101:FGSPISEKDAPALHKLLTNMIEDAGDLATRGACEKYMRI RPF AFYGVSTC	150
M. morgani	101:FGYPITEKDSPELYKLLTNMIEDAGDLATRSACEHYMRI RPF AFYGTETC	150
P. stuartii	101:FGYPITEKDAPEIHKLLTNMIEDAGDLATRSACEKYMRI RPF AFYGVATC	150
S. ficaria	97:FGLEIAQRKTPELFKLVMMKREDAGDLATRSACKNHYMRI RPF AFYNEATC	146
	** * * * *	
E. aerogenes	151:NTTEQDKLSKNGSYPSGHTSIGWATALVLAEINPQRQNEILKRGYELGES	200
E. blattae	151:NTTEQDKLSKNGSYPSGHTSIGWATALVLAEINPQRQNEILKRGYELGQS	200
K. planticola	151:NTTEQDKLSKNGSYPSGHTSIGWATALVLAEINPQRQNEILKRGYELGES	200
M. morgani	151:NTKDQKKLSTNGSYPSGHTSIGWATALVLAEYNPANQDAILRGYQLGQS	200
P. stuartii	151:NTKDQDKLSKNGSYPSGHTAIGWASALVLEINPENQDKILKRGYELGQS	200
S. ficaria	147:RPDEESTLSKNGSYPSGHTTIGWATALVLAEINPARQGEILQRGYDMGQS	196
	** * * * *	
E. blattae	201:RVICGYHWQSDVDAAARVVGSAVVATLHTNPAFQQQLQKAKAEFAQHQQK	249
K. planticola	201:RVICGYHWQSDVDAAARIVGSAVVATLHTNPAFQQQLQKAKDEFAKQKK-	248
M. morgani	201:RVICGYHWQSDVDAAARIVGSAAYATLHSDPAFQAQLAKAKQEFQKSSQK	249
E. aerogenes	201:RVICGYHWQSDVDAAARIVGSAVVATLHTNPAFQQQLQKAKDEFAKTQK-	248
P. stuartii	201:RVICGYHWQSDVDAAARIVASGAVATLHSNPEFQKQLQKAKDEFA-KLKK	248
S. ficaria	197:RVICGYHWQSDVTAARMAASAMVARLHAETFAAQLQKAKDEF-NGLKK	244
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